REMARKS

Claims 12, 14-20 and 31-34 are amended. Claim 35 is added. Claims 22-30 have been withdrawn from consideration by the Examiner. Claims 12-14, 16-21 and 31-35 are active and under consideration.

At the outset, Applicants wish to thank Examiner Marvich for the helpful and courteous discussion conducted with their U.S. representative, on March 17, 2009. The supporting remarks for patentability are consistent with the remarks made during the discussion with the Examiner.

Claims 12-15, 19-21 and 31-34 stand rejected under 35 USC 102(b) as being anticipated by *Poquet et al*, J. Bacteriology, 1998, Vol. 180, pages 1904-1912.

However, this reference fails to disclose or suggest the claimed invention.

Notably, *Poquet et al* (J. Bacteriology, 1998, Vol. 180: 1904-1912) disclose a plasmid pFUN comprising sequence accession number GenBank U95834 which contains the sequence named nlp3 (see attached copy of NCBI description of GenBank U95834). The sequence accession number U95834 consists of:

i) p_{Zn} promoter;

ii) a sequence encoding ZitR; and

iii) part of sequence coding for ZitS.

This sequence has been cloned in the polylinker of pFUN as to obtain expression of a fusion peptide n1p3/ΔNuc. Therefore, *Poquet et al* disclose a plasmid containing the p_{Zn} promoter (promoter sequence corresponding to SEQ ID NO: 1 of claimed expression cassette), a sequence encoding ZitR, the N-terminal part of ZitS fused with the sequence coding for ΔNuc, followed by the downstream restriction sites of the polylinker.

Amended claims 12 and 15 clearly relate to an expression cassette which does not contain

a sequence encoding any part of L. lactis **ZitS**. Consequently, the amended claims are clearly not anticipated by *Poquet et al.*

It is also clear that *Poquet et al* would have failed to have rendered the claimed invention obvious at the time it was made. *Poquet et al* identified among others a sequence (U95834 GenBank sequence) which contains n1p3 coding sequence. *Poquet et al* are only interested in exported peptide n1p3, and are totally silent about a possible function of the other nucleotide sequences contained in U95834 GenBank sequence. Nothing in the disclosure of *Poquet et al* or in accession number U95834 report would have suggested to the artisan that any other sequences contained in U95834 sequence could have a regulating function or code for a protein. See the attached NCBI description of GenBank U95834.

Therefore the person skilled in the art would not have been motivated to isolate specifically the nucleotide sequence corresponding to p_{Zn} promoter and sequence encoding ZitR from sequence GenBank accession number U95834 in order to engineer an expression cassette which has the characteristic to regulate expression of a gene according to the concentration of zinc in the culture medium.

Further, *Poquet et al* would not have enabled one skilled in the art to do so in any event.

Hence, this ground of rejection is unsustainable and should be withdrawn.

Claims 12-21 and 31-34 stand rejected under 35 USC 112, first paragraph, as the present specification ostensibly does not provide enablement for any embodiment of expression cassettes other than that containing SEQ ID NO: 1 operably linked to nucleotides 357-794 of SEQ ID NO: 2 further operably linked to a restriction site.

However, it is believed that the present claims are fully enabled by the present specification for the following reasons. The comments set forth below refer to Annex 1 and Annex 2, copies of

which are attached to this response.

First, the definition "at least 80% identity with the *Lactococcus lactis* ZitR protein GENBANK AAK06214" does not encompass a broad variety of proteins.

Second, Annex 1 shows the results of a BLAST search performed against the nr database which includes all the known protein sequences of all living organisms. Among these sequences, the only ones which share at least 80% identity with ZitR of L. *lactis* subsp. Lactis II1403 (GenBank AAK06214) are ZitR proteins, namely the ZitR protein of L. *lactis* subsp. *cremoris* MG1363 (88% identity) and the ZitR protein of L. *lactis* subsp. *cremoris* SK11 (89% identity). As a matter of fact there is no protein having at least 80% identity with GenBank AAK06214 which is not a ZitR protein. The next proteins which have the higher homology with ZitR are Streptococcus proteins which have at most 54% identity with GenBank AAK06214. Therefore, it is very unlikely that one can isolate a protein having 80% identity or more with GenBank AAK06214 which is not a ZitR protein.

Annex 2 shows the results of a BLAST search performed against the whole genome sequences of L. *lactis* subsp. Lactis II1403, L. *lactis* subsp. *cremoris* MG1363 and L. *lactis* subsp. *cremoris* SK11. There is no lactococcal protein, other than the ZitR proteins, having more than 38% identity with GenBank AAK06214.

Therefore using a probe derived from the sequence encoding GenBank AAK06214, or from nucleotides 357 to 794 of SEQ ID NO:9 of the instant application for screening a lactococcal DNA library, one of skill in the art would be able to easily discriminate a sequence encoding a ZitR protein from other lactococcal sequences.

Moreover, only the whole genome sequence of L. *lactis* subsp. Lactis Il1403 (which was published in 2001) was available before the invention was made. The genome sequences of *Lactococcus lactis* subsp. *cremoris* SK11 and *Lactococcus lactis* subsp. *cremoris* MG1363 were only available in GenBank in 2006 and 2007 respectively. It is pointed out, however, that besides indicating GenBank AAK06214 as the reference sequence for a ZitR protein, the present application discloses another sequence encoding a ZitR protein, namely nucleotides 357 to 794 of SEQ ID NO:9, which encodes the ZitR protein of *lactis* subsp. *cremoris* MG1363.

Actually, the knowledge of the lactococcal genome sequences is not necessary to practice the claimed invention. As indicated above, one of ordinary skill in the art could have easily obtained polynucleotides encoding lactococcal ZitR proteins by screening a DNA library of a *Lactococcus* with a probe derived from the sequence encoding GenBank AAK06214, or from nucleotides 357 to 794 of SEQ ID NO:9.

BLAST results are provided herewith solely to evidence that the lactococcal genome does not contain any protein having more than 80% identity with GenBank AAK06214 which is not a ZitR protein.

Second, the two BLAST searches and results thereof noted above indicate that the present specification does in fact satisfy both the statutory enablement requirement under 35 USC 112, first paragraph, and the case law tests therefor cited by the Examiner.

Specifically, under the case law tests for enablement articulated in In re Wright and In re Fisher, cited by the Examiner, it is clear that since nucleotide sequences having more than 80% identity with GENBANK AAK06214 could easily be obtained by routine screening with a probe (as described above), undue experimentation would not be required.

Claims 12-16, 18-20 and 31-34 are objected to.

However, in view of the above claim amendments, this ground of rejection is deemed moot.

The specification stands objected to.

However, attached to this response is a Substitute Specification which meets the requirements of 37 CFR 1.77(b).

Finally, Applicants hereby respond to the specific assertions set forth in the Notice of Non-Compliance of July 7, 2009.

First, claims 16, 18 and 20 have been amended as suggested by the Examiner. Claim 13 has been corrected.

Second, it is urged respectfully that claim 15 is not a duplicate of Claim 12. Notably claim 15 does not require element b) of claim 12, i.e., a sequence encoding a polypeptide with at least 80% identity with the *Lactococcus lactis* Zit R protein, placed under the transcriptional control of the promoter, and wherein the polypeptide is obtained from Lactococcus.

Third, Applicants have, in fact, addresses the rejection of claims 12-21 and 31-34 under 35 USC 112, first paragraph. See preceding pages 10-12 of this Amendment, wherein it is explained why these claims are enabled by the present specification.

CONCLUSION

Accordingly, in view of all of the above, it is believed that this application is now in condition for allowance. Early notice to this effect is earnestly solicited.

Applicant hereby petitions for the Commissioner to charge any additional fees or any underpayment of fees which may be required to maintain the pendency of this case or credit any overpayment to Deposit Account No. 14-0112.

Respectfully submitted,
THE NATH LAW GROUP

William E. Beaumont
Registration No. 30,996
Customer No. 20529

Date: April 7, 2009
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WEB/get

NCBI description of GenBank U95834

GenBank: U95834.1

Lactococcus lactis putative lipoprotein Nlp3 precursor, gene, partial cds

Features Sequence

```
LOCUS       LLU95834                 945 bp    DNA
linear   BCT 24-APR-1998
DEFINITION  Lactococcus lactis putative lipoprotein Nlp3
precursor, gene,
            partial cds.
ACCESSION   U95834
VERSION     U95834.1  GI:3043865
KEYWORDS    .
SOURCE      Lactococcus lactis subsp. cremoris MG1363
  ORGANISM  Lactococcus lactis subsp. cremoris MG1363
            Bacteria; Firmicutes; Lactobacillales;
Streptococcaceae;
            Lactococcus.
REFERENCE   1  (bases 1 to 945)
  AUTHORS   Poquet,I., Ehrlich,S.D. and Gruss,A.
  TITLE     An export-specific reporter designed for gram-
positive bacteria:
            application to Lactococcus lactis
  JOURNAL   J. Bacteriol. 180 (7), 1904-1912 (1998)
   PUBMED   9537391
REFERENCE   2  (bases 1 to 945)
  AUTHORS   Poquet,I. and Gruss,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAR-1997) Laboratoire de Genetique
Appliquee-URLGA,
            Institut National de la Recherche Agronomique,
CRJ, Jouy en Josas
            78352, France
FEATURES             Location/Qualifiers
     source          1..945
                     /organism="Lactococcus lactis subsp.
cremoris MG1363"
                     /mol_type="genomic DNA"
                     /strain="MG1363"
                     /db_xref="taxon:416870"
     CDS             complement(<1..330)
                     /note="identified as a fusion to a
signal peptide-less
                     form of the staphylococcal nuclease
reporter which
                     displays nuclease activity; similar to
S. pneumoniae
                     adhesion protein, Swiss-Prot Accession
Number P42363"
```

Change Region Shown

Customize View

Pick Primers
Design and test primers for this sequence using Primer-BLAST.

Recent Activity

Turn Off Clear

Lactococcus lactis putative lipoprotein

U95834 (1) Nucleotide

All links from this record

Full text in PMC
Protein
PubMed
Taxonomy
Related Sequences

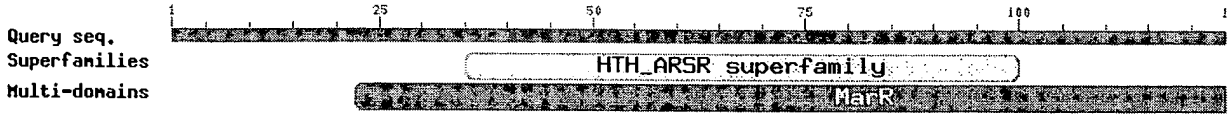
```
                     /codon_start=1
                     /transl_table=11
                     /product="putative lipoprotein Nlp3
precursor"
                     /protein_id="AAC14602.1"
                     /db_xref="GI:3043866"
                     /translation="MKKILMLFAIPAVLLLAGCQKTADKP
EVVTTFEPMYEFTKAIVG

DKVKIENIVPANQEVHEFEPSAKQVATMTNAQAIIYNSDDLEKWALKVNNKGVKIEAS
                     KDVNKIKG"
     sig_peptide     complement(277..330)
                     /note="encodes lipoprotein-type signal
peptide"
     mat_peptide     complement(<1..276)
                     /product="putative lipoprotein Nlp3"
ORIGIN
        1 tcctttaatt ttattgacat ctttgcttgc ttctattttg
actcctttat tattcacttt
       61 cagagcccat ttttcaaggt catcagaatt ataaataata
gcttgagcat ttgtcattgt
      121 tgcaacttgc ttggcactcg gttcaaattc gtgaacttct
tgattcgccg gaacaatatt
      181 ttcaatttta accttatctc caacaatcgc tttcgtaaat
tcatacatcg gctcaaaagt
      241 tgtcacaact tctggtttgt ctgctgtttt ttgacaacca
gcaagaagta aaactgccgg
      301 aatagcaaat aacatcaata ttttcttcat cgaaactcct
ccgtaagtac tgataagaat
      361 tgacttatca ctttttgttc ttcgtcagta aatttgtctc
ctaattcttg gtaggtactt
      421 agagttttct catgatgagc agcatgttct ttagcaactg
gaattgcttt ttctgtcagg
      481 ctccaaagga ctacgcgttc gtcatttgtt gcccgacttg
atttaatcag ttcttgctct
      541 tgtaattttt tgagagcttt agttaccgct gctggcgaaa
tcttgagttg ctcggcaatt
      601 ctcgcgtttg tcgaaacctc tgcagctaga atcattaaga
tatgttcttg cgtgcttgtt
      661 agcttaacat tactttngca ttcgccgagt aatatttcat
gcttgttttn tgcaaactgc
      721 ataattgccc caagaaactg gtcgatttga tttgctaaan
tcatagtatt ttgtcctcca
      781 taattagttt actggttaat tatatagcaa agtaaaaata
atgtcaacca gttaacatta
      841 ttttttactt ttttatttga aaaatccttc catccttaag
ccgaacatca aaacaataag
      901 ttttattact aacagtttga ccaccgctag ttgaaccagc tgaca
//
```

Annex 1

Length adjustment	109
Effective length of query	36
Effective length of database	1873821432
Effective search space	67457571552
Effective search space used	67457571552

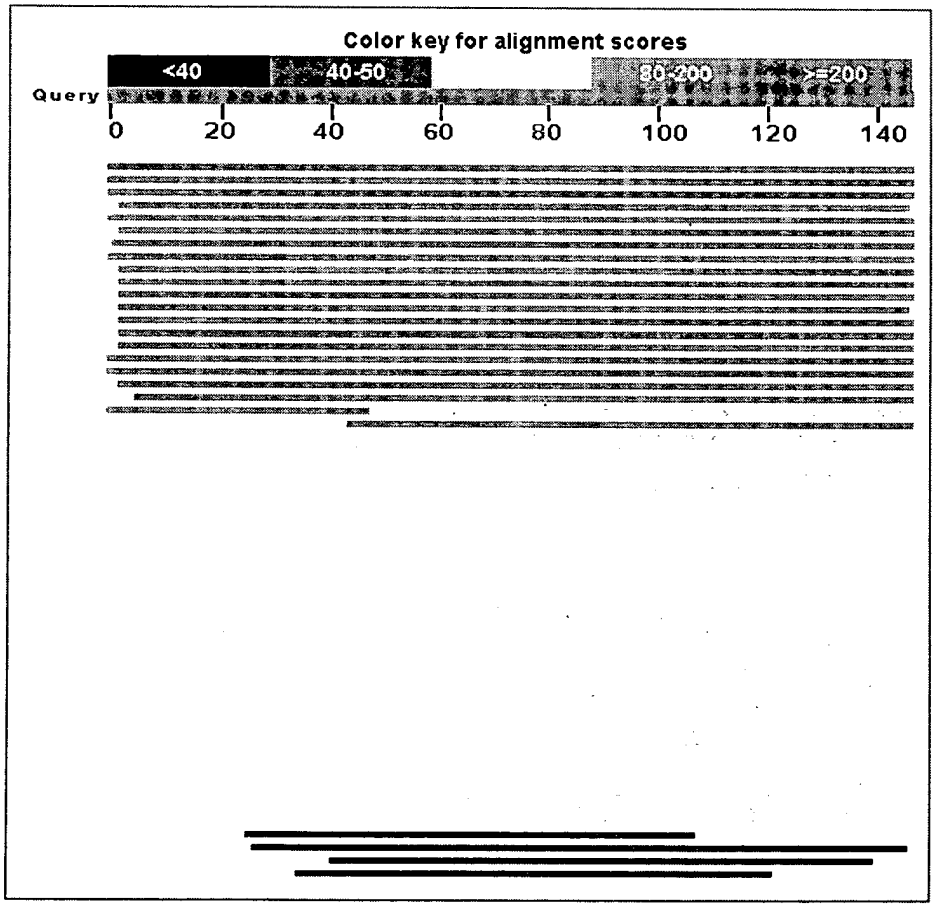
Graphic Summary
Show Conserved Domains
Putative conserved domains have been detected, click on the image below for detailed results.



Distribution of 100 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



Annex 1

Descriptions

Sequences producing significant alignments:	Score (Bits)	E Value	
ref|NP_266273.1| zinc transport transcription regulator [Lact...	291	1e-77	G
ref|YP_81478.1| transcriptional regulator [Lactococcus lacti...	262	1e-70	G
ref|YP_001033643.1| transcriptional regulator of the zit oper...	262	2e-70	G
ref|YP_001034147.1| multiple antibiotic resistance operon tra...	154	2e-36	G
ref|NP_372293.1| putative transcriptional regulator [Streptoc...	145	1e-33	G
ref|YP_002122433.1| transcriptional repressor AdcR for Zn(2+)...	143	3e-33	G
ref|NP_806407.1| putative repressor protein [Streptococcus py...	141	1e-32	G
ref|ZP_02920034.1| hypothetical protein STRINF_00865 [Strepto...	141	2e-32	
ref|NP_268489.1| putative repressor protein [Streptococcus py...	138	2e-32	G
ref|YP_002551480.1| MarR-family regulatory protein [Streptoco...	135	1e-31	G
ref|NP_687190.1| adc operon repressor AdcR [Streptococcus aga...	134	5e-31	G
ref|YP_001141295.1| repressor protein adcR [Streptococcus gor...	133	4e-30	G
ref|ZP_01917760.1| adc operon repressor AdcR [Streptococcus p...	132	6e-30	
ref|NP_359264.1| adc operon repressor AdcR [Streptococcus pne...	131	2e-29	G
ref|NP_346656.1| adc operon repressor AdcR [Streptococcus pne...	130	2e-29	G
ref|YP_138725.1| zinc transport transcriptional repressor [St...	129	5e-29	G
ref|YP_819746.1| zinc transport transcriptional repressor [St...	128	1e-28	G
ref|YP_002743974.1| transcriptional regulator [Streptococcus ...	116	7e-25	G
ref|ZP_03825066.1| transcriptional regulator, MarR family [St...	110	4e-23	
emb|CAA75212.1| hypothetical protein [Lactococcus lactis subs...	97.4	1e-17	
ref|ZP_01302472.1| COG1846: Transcriptional regulators [Strep...	96.3	3e-17	
ref|YP_001486469.1| MarR family transcriptional regulator [Ba...	67.0	5e-10	G
ref|YP_001198872.1| transcriptional regulator [Streptococcus ...	63.2	6e-09	G
ref|YP_187016.1| MarR family transcriptional regulator [Staph...	63.2	7e-09	G
ref|YP_001777375.1| transcriptional repressor for Zn(2+)-resp...	62.8	8e-09	G
ref|YP_001317...| hypothetical protein SAOUHSC_02819 [Staphylo...	62.8	8e-09	G
ref|ZP_03963431.1| MarR family transcriptional regulator [Sta...	61.2	3e-08	
ref|YP_174460.1| MarR family transcriptional regulator [Bacil...	60.5	4e-08	G
ref|xP_080661.1| transcriptional regulator YvnA [Bacillus lic...	58.3	1e-07	G
ref|YP_254003.1| hypothetical protein pSHaeC05 [Staphylococcu...	58.3	1e-07	G
ref|YP_092087.1| YvnA [Bacillus licheniformis ATCC 14580] >gb...	58.3	1e-07	G
ref|ZP_00728634.1| Transcriptional regulator, MarR family [Ba...	55.8	9e-07	
ref|ZP_02613091.1| transcriptional regulator, MarR family [Cl...	54.3	3e-06	
ref|YP_001153547.1| MarR family transcriptional regulator [Cl...	54.3	3e-06	G
ref|YP_001760642.1| MarR family transcriptional regulator [Cl...	54.3	3e-06	G
ref|YP_001055331.1| MarR family transcriptional regulator [La...	53.9	4e-06	G
ref|ZP_02617530.1| transcriptional regulator, MarR family [Cl...	53.9	4e-06	
ref|YP_861960.1| MarR family transcriptional regulator [Grame...	53.9	4e-06	G
ref|NP_391388.1| hypothetical protein BSU35080 [Bacillus subt...	53.5	5e-06	G
ref|ZP_02994615.1| hypothetical protein CLOSPO_01734 [Clostri...	53.5	6e-06	
ref|ZP_01994132.1| hypothetical protein DORLON_00120 [Dorea l...	53.1	6e-06	
ref|ZP_03294054.1| hypothetical protein CLOHIR_02015 [Clostri...	53.1	7e-06	
ref|ZP_02211336.1| hypothetical protein CLOBAR_00939 [Clostri...	52.4	1e-05	
ref|YP_001390364.1| MarR family transcriptional regulator [Cl...	52.4	1e-05	G
ref|YP_001756407.1| MarR family transcriptional regulator [Cl...	51.6	2e-05	G
ref|YP_809775.1| transcriptional regulator [Lactococcus lacti...	51.2	2e-05	G
ref|YP_001638248.1| MarR family transcriptional regulator [Ly...	51.2	3e-05	G
ref|NP_266864.1| transcription regulator [Lactococcus lactis ...	51.2	3e-05	G
ref|ZP_01723095.1| transcriptional regulator, MarR family pro...	50.8	4e-05	
ref|xP_808147.1| transcriptional regulator [Lactococcus lacti...	50.4	5e-05	G
ref|NP_786292.1| transcription regulator [Lactobacillus plant...	50.1	6e-05	G
ref|YP_757477.1| MarR family transcriptional regulator [Maric...	50.1	6e-05	G
ref|NP_391385.1| hypothetical protein BSU35050 [Bacillus subt...	50.1	6e-05	G
ref|NP_111681.1| transcription regulator (SlyA-related) [Ther...	49.7	7e-05	G
ref|NP_419215.1| MarR family transcriptional regulator [Caulo...	49.3	9e-05	G
ref|YP_001031465.1| MarR family transcriptional regulator [La...	49.3	1e-04	G
ref|NP_603578.1| MarR family transcriptional regulator [Fusob...	48.9	1e-04	G
ref|YP_138915.1| MarR family transcriptional regulator [Strep...	48.9	1e-04	G
ref|YP_001165566.1| possible MarR family transcriptional regu...	48.9	1e-04	G
ref|ZP_03144611.1| Transcriptional regulator, MarR family [Fu...	48.9	1e-04	

Annex 1

BLAST Basic Local Alignment Search Tool

•

Edit and Resubmit Save Search Strategies Formatting options Download

gb|AAK06214| (145 letters)

Results for: gb|AAK06214.1 zinc transport transcriptional regulator [Lactococcus lactis subsp. lactis Il1403](145aa)
Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID
gi|12725171|gb|AAK06214.1|AE006439_11
Description
zinc transport transcriptional regulator [Lactococcus lactis subsp. lactis Il1403]
Molecule type
amino acid
Query Length
145

Database Name
nr
Description
All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program
BLASTP 2.2.19+ Citation

Reference
Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.
Reference - compositional score matrix adjustment
Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.
Other reports: Search Summary [Taxonomy reports] [Distance tree of results]

Search Parameters

Program	blastp
Word size	3
Expect value	10
Hitlist size	100
Gapcosts	11,1
Matrix	BLOSUM62
Threshold	11
Composition-based stats	2
Filter string	F
Genetic Code	1
Window Size	40

Database

Posted date	Mar 2, 2009 5:57 PM
Number of letters	2,739,991,458
Number of sequences	7,946,514
Entrez query	none

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.310848	0.267
K	0.124161	0.041
H	0.32399	0.14

Results Statistics

Annex 1

ref|YP_819912.1|	MarR family transcriptional regulator [Strep...	48.9	1e-04 G
ref|YP_079349.1|	transcriptional regulator YvmB [Bacillus lic...	48.5	2e-04 G
ref|ZP_01218563.1|	putative transcriptional regulator, MarR f...	48.1	2e-04
ref|YP_091766.1|	YvmB [Bacillus licheniformis ATCC 14580] >gb...	48.1	2e-04 G
ref|YP_129221.1|	MarR family transcriptional regulator [Photo...	48.1	2e-04 G
ref|ZP_00990845.1|	hypothetical transcriptional regulator, Ma...	48.1	2e-04
ref|YP_001218891.1|	MarR family transcriptional regulator [Al...	47.8	3e-04 G
ref|YP_001826502.1|	MarR family transcriptional regulator [Le...	47.8	3e-04 G
ref|YP_196511.1|	putative transcriptional regulatory protein ...	47.4	4e-04 G
ref|YP_001361560.1|	Transcriptional regulator, marR family [L...	47.4	4e-04 G
ref|YP_001510774.1|	MarR family transcriptional regulator [Cl...	47.4	4e-04 G
ref|ZP_02386568.1|	hypothetical transcriptional regulator, Ma...	47.0	5e-04
ref|YP_140799.1|	MarR family transcriptional regulator [Strep...	47.0	5e-04 G
ref|YP_142999.1|	MarR family transcriptional regulator [Therm...	46.6	6e-04 G
ref|YP_293871.1|	regulatory protein, MarR [Ralstonia eutropha...	46.6	7e-04 G
ref|YP_001707422.1|	MarR family transcriptional regulator [Cl...	46.6	7e-04 G
ref|ZP_02956515.1|	transcriptional regulator, MarR family [Cl...	46.2	8e-04
ref|NP_268269.1|	transcription regulator [Lactococcus lactis ...	46.2	0.001 G
ref|YP_001325439.1|	transcriptional regulator, MarR family [D...	46.2	0.001 G
ref|ZP_01854755.1|	probable marR-family transcription regulat...	46.2	0.001
ref|YP_774[illegible].1|	MarR family transcriptional regulator [Burkh...	46.0	0.001 G
ref|ZP_01451766.1|	transcriptional regulator, MarR family pro...	45.8	0.001
ref|ZP_01623ad3.1|	transcriptional regulator, MarR family [Ba...	45.8	0.001
ref|YP_002467443.1|	transcriptional regulator, MarR family [C...	45.8	0.001 G
ref|ZP_02[illegible]|	hypothetical protein BLAHAN_01259 [Blautia...	45.4	0.001
ref|ZP_02891041.1|	transcriptional regulator, MarR family [Bu...	45.4	0.001
ref|YP_001808132.1|	MarR family transcriptional regulator [Bu...	45.4	0.001 G
ref|ZP_02906201.1|	transcriptional regulator, MarR family [Bu...	45.4	0.001
ref|ZP_02367996.1|	transcriptional regulator, MarR family pro...	45.4	0.001
ref|NP_377055.1|	MarR family transcriptional regulator [Bacil...	45.4	0.002 G
ref|NP_782475.1|	MarR family transcriptional regulator [Clost...	45.4	0.002 G
ref|ZP_03570809.1|	transcriptional regulator, MarR family [Bu...	45.1	0.002
ref|YP_001119315.1|	MarR family transcriptional regulator [Bu...	45.1	0.002 G
ref|YP_002418276.1|	Histone acetyltransferase HPA2 and relate...	45.1	0.002 G
ref|ZP_02355842.1|	transcriptional regulator, MarR family pro...	45.1	0.002
ref|YP_443675.1|	MarR family transcriptional regulator [Burkh...	44.7	0.002 G
ref|ZP_02633996.1|	transcriptional regulator, MarR family [Cl...	44.7	0.002
ref|YP_001374721.1|	MarR family transcriptional regulator [Ba...	44.7	0.002 G
ref|YP_819861.1|	transcriptional regulator [Leuconostoc mesen...	44.7	0.002 G
ref|ZP_02027443.1|	hypothetical protein EUBVEN_02713 [Eubacte...	44.7	0.003

Alignments Select All Get selected sequences Distance tree of results

>ref|NP_268273.1| G zinc transport transcription regulator [Lactococcus lactis subsp. lactis Il1403]

gb|AAK06214.1|AE006439_11 G zinc transport transcriptional regulator [Lactococcus lactis subsp. lactis Il1403]
Length=145

GENE ID: 1115793 zitR | zinc transport transcription regulator [Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 291 bits (744), Expect = 1e-77, Method: Compositional matrix adjust.
Identities = 145/145 (100%), Positives = 145/145 (100%), Gaps = 0/145 (0%)

```
Query  1    MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL  60
            MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL
Sbjct  1    MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL  60

Query  61   KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE  120
            KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE
Sbjct  61   KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE  120

Query  121  LGNKFTDEEQEVISKFLSALTEEFQ  145
            LGNKFTDEEQEVISKFLSALTEEFQ
Sbjct  121  LGNKFTDEEQEVISKFLSALTEEFQ  145
```

>ref|YP_811979.1| G transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]

gb|ABJ73866.1| G Transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
Length=145

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GENE ID: 4433026 LACR_2420 | transcriptional regulator
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 268 bits (685), Expect = 1e-70, Method: Compositional matrix adjust.
Identities = 130/145 (89%), Positives = 141/145 (97%), Gaps = 0/145 (0%)

```
Query  1    MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL  60
            MSLANQIDQFLG IMQFAENKHEILLG+CES+VKLTSTQEHILM+LA ++STNA+IAE+L
Sbjct  1    MSLANQIDQFLGAIMQFAENKHEILLGECESNVKLTSTQEHILMILAAEVSTNARIAEQL  60

Query  61   KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE  120
            KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHA HHEKTLSTYQE
Sbjct  61   KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHAAHHEKTLSTYQE  120

Query  121  LGNKFTDEEQEVISKFLSALTEEFQ  145
            LG+KFTDEEQ+VIS+FLS LTEEF+
Sbjct  121  LGDKFTDEEQKVISQFLSVLTEEFR  145
```

>ref|YP_001033643.1| transcriptional regulator of the zit operon [Lactococcus lactis subsp. cremoris MG1363]
emb|CAL98965.1| transcriptional regulator of the zit operon [Lactococcus lactis subsp. cremoris MG1363]
Length=145

GENE ID: 4799067 zitR | transcriptional regulator of the zit operon
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 267 bits (682), Expect = 2e-70, Method: Compositional matrix adjust.
Identities = 129/145 (88%), Positives = 141/145 (97%), Gaps = 0/145 (0%)

```
Query  1    MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL  60
            MSLANQIDQFLG IMQFAENKHEILLG+CES+VKLTSTQEHILM+LA ++STNA+IAE+L
Sbjct  1    MSLANQIDQFLGAIMQFAENKHEILLGECESNVKLTSTQEHILMILAAEVSTNARIAEQL  60

Query  61   KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE  120
            KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKA+PVAKEHAAHHEKTLSTYQE
Sbjct  61   KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAIPVAKEHAAHHEKTLSTYQE  120

Query  121  LGNKFTDEEQEVISKFLSALTEEFQ  145
            LG+KFTDEEQ+VIS+FLS LTEEF+
Sbjct  121  LGDKFTDEEQKVISQFLSVLTEEFR  145
```

>ref|YP_001034147.1| multiple antibiotic resistance operon transcriptional repressor (MarR), putative [Streptococcus sanguinis SK36]
gb|ABN43597.1| Multiple antibiotic resistance operon transcriptional repressor (MarR), putative [Streptococcus sanguinis SK36]
Length=147

GENE ID: 4806188 adcR | multiple antibiotic resistance operon transcriptional repressor (MarR), putative [Streptococcus sanguinis SK36]
(10 or fewer PubMed links)

Score = 154 bits (389), Expect = 2e-36, Method: Compositional matrix adjust.
Identities = 78/142 (54%), Positives = 102/142 (71%), Gaps = 0/142 (0%)

```
Query  3    LANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKI  62
            LA +IDQFL  ++  AEN+HEIL+G C SDV LT+TQEHILMLL+E+  TN+ +A+KL +
Sbjct  4    LAQKIDQFLNEVILKAENQHEILIGSCTSDVPLTNTQEHILMLLSEESLTNSDLAKKLNV  63

Query  63   SPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELG  122
            S AAVTKA+K L  QE++++ +   D RV  + LTE A P+AKEH  HH  TL TYQ+L
Sbjct  64   SQAAVTKAVKSLARQEMLQAFKDKRDARVTFYRLTELAQPIAKEHQHHHAHTLETYQKLA  123

Query  123  NKFTDEEQEVISKFLSALTEEF  144
             +F+  EQ VI+KFL AL  E
Sbjct  124  EQFSASEQAVIAKFLEALVGEI  145
```

>ref|NP_722293.1| putative transcriptional regulator [Streptococcus mutans UA159]
gb|AAN59599.1|AE015022_6 putative transcriptional regulator [Streptococcus mutans UA159]
Length=148

GENE ID: 1029245 SMU.1995c | putative transcriptional regulator
[Streptococcus mutans UA159] (10 or fewer PubMed links)

Score = 145 bits (365), Expect = 1e-33, Method: Compositional matrix adjust.
Identities = 76/146 (52%), Positives = 105/146 (71%), Gaps = 1/146 (0%)

```
Query  1    MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQIS-TNAKIAEK  59
            M+L  QID  +  I+  AEN HE+L+G C+SDVKLT+TQEHILMLL+++ S TN+ +A++
Sbjct  1    MTLGQQIDALINQIILKAENHHELLIGSCQSDVKLTNTQEHILMLLSQEKSLTNSDLAKE  60

Query  60   LKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQ  119
            L IS AAVTKA+K L  QE+++  +   D RV  + LT+ A PVAKEH  HH  TLS Y
Sbjct  61   LNISQAAVTKAVKSLVGQEMLELIKDGTDARVTYFRLTKLAEPVAKEHEHHHVATLSVYD  120

Query  120  ELGNKFTDEEQEVISKFLSALTEEFQ  145
             +  KF+ +E+ VIS+FL+ALT+E +
Sbjct  121  RISQKFSQKEKSVISRFLTALTKELE  146
```

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>**ref|YP_002122498.1|** transcriptional repressor AdcR for Zn(2+)-responsive expression [Streptococcus equi subsp. zooepidemicus MGCS10565]
gb|ACG61485.1| transcriptional repressor AdcR for Zn(2+)-responsive expression [Streptococcus equi subsp. zooepidemicus MGCS10565]
Length=147

GENE ID: 6760627 adcR | transcriptional repressor AdcR for Zn(2+)-responsive expression [Streptococcus equi subsp. zooepidemicus MGCS10565]

Score = 143 bits (361), Expect = 3e-33, Method: Compositional matrix adjust.
Identities = 70/143 (48%), Positives = 102/143 (71%), Gaps = 0/143 (0%)

```
Query  3    LANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKI  62
            L  ++D  +  I+  AEN+HE+L G C+SDVKLT+TQEHILMLL+++  TN  +A++L I
Sbjct  4    LEKKLDNLVNRILLKAENQHELLFGACQSDVKLTNTQEHILMLLSQEKLTNTDLAKRLNI  63

Query  63   SPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELG  122
            S AAVTKA+K L +QE++  ++ T D RV  + LT+ A P+AKEH  HH+KTL+ Y  L
Sbjct  64   SQAAVTKAIKGLIKQEMLAGTKDTVDARVTYFELTDLARPIAKEHTHHHDKTLAVYHRLL  123

Query  123  NKFTDEEQEVISKFLSALTEEFQ  145
              F+ EEQ ++ KF++A +EE +
Sbjct  124  AHFSAEEQVIVEKFITAFSEELE  146
```

>**ref|NP_606407.1|** putative repressor protein [Streptococcus pyogenes MGAS8232]
ref|NP_663873.1| putative repressor protein [Streptococcus pyogenes MGAS315]
ref|NP_801332.1| putative repressor protein [Streptococcus pyogenes SSI-1]
20 more sequence titles

ref|YP_059443.1| MarR family transcriptional regulator [Streptococcus pyogenes MGAS10394]
ref|YP_279544.1| MarR family transcriptional regulator [Streptococcus pyogenes MGAS6180]
ref|YP_595809.1| MarR family transcriptional regulator [Streptococcus pyogenes MGAS9429]
ref|YP_597688.1| MarR family transcriptional regulator [Streptococcus pyogenes MGAS10270]
ref|YP_599676.1| MarR family transcriptional regulator [Streptococcus pyogenes MGAS2096]
ref|YP_601578.1| Transcriptional regulator, MarR family [Streptococcus pyogenes MGAS10750]
ref|YP_001127671.1| MarR family regulatory protein [Streptococcus pyogenes str. Manfredo]
ref|YP_002285129.1| Putative repressor protein [Streptococcus pyogenes NZ131]
sp|Q5XEA3.1|ADCR_STRP6 RecName: Full=Transcriptional repressor adcR
gb|AAL96906.1| putative repressor protein [Streptococcus pyogenes MGAS8232]
gb|AAM78676.1| putative repressor protein [Streptococcus pyogenes MGAS315]
dbj|BAC63165.1| putative repressor protein [Streptococcus pyogenes SSI-1]
gb|AAT86260.1| Transcriptional regulator, MarR family [Streptococcus pyogenes MGAS10394]
gb|AAX71189.1| transcriptional regulator, MarR family [Streptococcus pyogenes MGAS6180]
gb|ABF31265.1| transcriptional regulator, MarR family [Streptococcus pyogenes MGAS9429]
gb|ABF33144.1| Transcriptional regulator, MarR family [Streptococcus pyogenes MGAS10270]
gb|ABF35132.1| Transcriptional regulator, MarR family [Streptococcus pyogenes MGAS2096]
gb|ABF37034.1| Transcriptional regulator, MarR family [Streptococcus pyogenes MGAS10750]
emb|CAM29417.1| MarR-family regulatory protein [Streptococcus pyogenes str. Manfredo]
gb|ACI60434.1| Putative repressor protein [Streptococcus pyogenes NZ131]
Length=147

GENE ID: 994164 adcR | putative repressor protein [Streptococcus pyogenes MGAS8232] (10 or fewer PubMed links)

Score = 141 bits (356), Expect = 1e-32, Method: Compositional matrix adjust.
Identities = 69/144 (47%), Positives = 101/144 (70%), Gaps = 0/144 (0%)

```
Query  2    SLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLK  61
            +L  ++D  + TI+  AEN+HE+L G C+SDVKLT+TQEHILMLL++Q  TN  +A+ L
Sbjct  3    TLEKKLDNLVNTILLKAENQHELLFGACQSDVKLTNTQEHILMLLSQQRLTNTDLAKALN  62

Query  62   ISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQEL  121
            IS AAVTKA+K L +Q+++  ++ T D RV  + LTE A P+A EH  HH++TL+ Y  L
Sbjct  63   ISQAAVTKAIKSLVKQDMLAGTKDTVDARVTYFELTELAKPIASEHTHHHDETLNVYNRL  122

Query  122  GNKFTDEEQEVISKFLSALTEEFQ  145
              KF+ +E E++ KF++   EE +
Sbjct  123  LQKFSAKELEIVDKFVTVFAEELE  146
```

>**ref|ZP_02920004.1|** hypothetical protein STRINF_00865 [Streptococcus infantarius

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subsp. infantarius ATCC BAA-102]
gb|EDT48012.1| hypothetical protein STRINF_00865 [Streptococcus infantarius subsp. infantarius ATCC BAA-102]
Length=148

Score = 141 bits (355), Expect = 2e-32, Method: Compositional matrix adjust.
Identities = 70/145 (48%), Positives = 103/145 (71%), Gaps = 0/145 (0%)

```
Query  1    MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL  60
            M L  QID  +  I+  AEN+HE+L G C+S V+LT+TQEHILMLL+++  TN+ +A++L
Sbjct  1    MQLEKQIDCLVNEILLKAENQHELLFGACQSGVELTNTQEHILMLLSQERLTNSALAKRL  60

Query  61   KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE  120
             IS AAVTKA+K L ++ ++   +  +D RV  + LTE A PVA EH  HH  TLS Y++
Sbjct  61   NISQAAVTKAIKCLVKEGMLAPVKNKDDARVTYFELTEFAKPVADEHNHHHHATLSVYKK  120

Query  121  LGNKFTDEEQEVISKFLSALTEEFQ  145
            + + F+DEEQ +IS+FL+A ++E +
Sbjct  121  MIDDFSDEEQSIISRFLTAFSDELE  145
```

>ref|NP_268489.1| putative repressor protein [Streptococcus pyogenes M1 GAS]
ref|YP_281441.1| MarR family transcriptional regulator [Streptococcus pyogenes MGAS5005]
gb|AAK33210.1| putative repressor protein [Streptococcus pyogenes M1 GAS]
gb|AAZ50696.1| transcriptional regulator, MarR family [Streptococcus pyogenes MGAS5005]
Length=147

GENE ID: 900432 adcR | putative repressor protein [Streptococcus pyogenes M1 GAS] (10 or fewer PubMed links)

Score = 141 bits (355), Expect = 2e-32, Method: Compositional matrix adjust.
Identities = 69/143 (48%), Positives = 100/143 (69%), Gaps = 0/143 (0%)

```
Query  3    LANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKI  62
            L  ++D  + TI+  AEN+HE+L G C+SDVKLT+TQEHILMLL++Q  TN  +A+ L I
Sbjct  4    LEKKLDNLVNTILLKAENQHELLFGACQSDVKLTNTQEHILMLLSQQRLTNTDLAKALNI  63

Query  63   SPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELG  122
            S AAVTKA+K L +Q+++   ++ T D RV  + LTE A P+A EH  HH++TL+ Y  L
Sbjct  64   SQAAVTKAIKSLVKQDMLAGTKDTVDARVTYFELTELAKPIASEHTHHHDETLNVYNRLL  123

Query  123  NKFTDEEQEVISKFLSALTEEFQ  145
             KF+ +E E++ KF++   EE +
Sbjct  124  QKFSAKELEIVDKFVTVFAEELE  146
```

>ref|YP_002561480.1| MarR-family regulatory protein [Streptococcus uberis 0140J]
emb|CAR40515.1| MarR-family regulatory protein [Streptococcus uberis 0140J]
Length=147

GENE ID: 7392663 SUB0110 | MarR-family regulatory protein [Streptococcus uberis 0140J]

Score = 138 bits (348), Expect = 1e-31, Method: Compositional matrix adjust.
Identities = 69/143 (48%), Positives = 102/143 (71%), Gaps = 0/143 (0%)

```
Query  3    LANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKI  62
            L ++IDQ +  I+  AEN+HE+L G C+S VKLT+TQEHILMLL+++  TN  +A+KL I
Sbjct  4    LESKIDQLVNQILLKAENQHELLFGACQSHVKLTNTQEHILMLLSQEQLTNTDLAKKLNI  63

Query  63   SPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELG  122
            S AAVTKA+K L + E++ + + T D RV  + LT  A P+A+EH  HH++TL+ Y +L
Sbjct  64   SQAAVTKAIKSLMKHEMLSAIKDTVDARVTYFELTPAAKPIAEEHTQHHDETLNVYTKLL  123

Query  123  NKFTDEEQEVISKFLSALTEEFQ  145
            + F+ EE+ VI KFL+  ++E +
Sbjct  124  SSFSSEEKAVIDKFLTVFSDELE  146
```

>ref|NP_687190.1| adc operon repressor AdcR [Streptococcus agalactiae 2603V/R]
ref|NP_734620.1| adc operon repressor AdcR [Streptococcus agalactiae NEM316]
ref|YP_328885.1| adc operon repressor AdcR [Streptococcus agalactiae A909]
13 more sequence titles

ref|ZP_00781732.1| repressor protein adcR [Streptococcus agalactiae 18RS21]
ref|ZP_00784062.1| adc operon repressor AdcR [Streptococcus agalactiae H36B]
ref|ZP_00786322.1| adc operon repressor AdcR [Streptococcus agalactiae COH1]
ref|ZP_00787320.1| adc operon repressor AdcR [Streptococcus agalactiae CJB111]
ref|ZP_00790981.1| adc operon repressor AdcR [Streptococcus agalactiae 515]
gb|AAM99062.1|AE014198_10 adc operon repressor AdcR [Streptococcus agalactiae 2603V/R]
emb|CAD45795.1| unknown [Streptococcus agalactiae NEM316]
gb|ABA46120.1| adc operon repressor AdcR [Streptococcus agalactiae A909]
gb|EAO61676.1| repressor protein adcR [Streptococcus agalactiae 18RS21]
gb|EAO70283.1| adc operon repressor AdcR [Streptococcus agalactiae 515]
gb|EAO73974.1| adc operon repressor AdcR [Streptococcus agalactiae CJB111]
gb|EAO74935.1| adc operon repressor AdcR [Streptococcus agalactiae COH1]
gb|EAO77202.1| adc operon repressor AdcR [Streptococcus agalactiae H36B]
Length=147

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GENE ID: 1012928 adcR | adc operon repressor AdcR
[Streptococcus agalactiae 2603V/R] (10 or fewer PubMed links)

Score = 136 bits (343), Expect = 5e-31, Method: Compositional matrix adjust.
Identities = 65/143 (45%), Positives = 99/143 (69%), Gaps = 0/143 (0%)

```
Query  3    LANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKI  62
            L  ++D  +  I+  AEN+HE+L G C+SDVKLT+TQEHILMLL+++  TN+ +A+KL I
Sbjct  4    LEQKLDHLVSQILLKAENQHELLFGTCQSDVKLTNTQEHILMLLSQEQLTNSDLAKKLNI  63

Query  63   SPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELG  122
            S AAVTKA+K L  Q+++K+++ + D R+  + L+E A P+A EH  HH+ TL  Y  L
Sbjct  64   SQAAVTKAVKSLISQDMLKANKDSKDARITYFELSELAKPIADEHTHHHDNTLGVYGRLV  123

Query  123  NKFTDEEQEVISKFLSALTEEFQ  145
            N F+ +E+ V+ +FL   + E +
Sbjct  124  NHFSKDEKVVLERFLDLFSRELE  146
```

>**ref|YP_001451205.1|** repressor protein adcR [Streptococcus gordonii str. Challis substr. CH1]
gb|AAO43167.1| putative transcriptional repressor; AdcR [Streptococcus gordonii subsp. challis]
gb|ABV10972.1| repressor protein adcR [Streptococcus gordonii str. Challis substr. CH1]
Length=147

GENE ID: 5599115 adcR | repressor protein adcR
[Streptococcus gordonii str. Challis substr. CH1] (10 or fewer PubMed links)

Score = 133 bits (335), Expect = 4e-30, Method: Compositional matrix adjust.
Identities = 75/142 (52%), Positives = 101/142 (71%), Gaps = 0/142 (0%)

```
Query  3    LANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKI  62
            LA++ID FL  I+  AEN+HEIL+G C S+V LT+TQEHILMLLAE++ TN+ +A+KL +
Sbjct  4    LAHKIDSFLNEIILKAENQHEILVGSCTSNVALTNTQEHILMLLAEEMLTNSDLAKKLNV  63

Query  63   SPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELG  122
            S AAVTKA+K L  Q ++++ +   D RV  + LTE A P+A EH  HH  TL TYQ L
Sbjct  64   SQAAVTKAVKSLINQGMLETFKDKKDARVTFYRLTELAQPIADEHEHHHAHTLETYQSLL  123

Query  123  NKFTDEEQEVISKFLSALTEEF  144
            ++F+ +EQ+ I KFL AL  E
Sbjct  124  DRFSQDEQQAIEKFLEALVGEI  145
```

>**ref|ZP_01817760.1|** adc operon repressor AdcR [Streptococcus pneumoniae SP3-BS71]
ref|YP_002512031.1| MarR-family regulatory protein [Streptococcus pneumoniae ATCC 700669]
gb|EDK74363.1| adc operon repressor AdcR [Streptococcus pneumoniae SP3-BS71]
emb|CAR69937.1| MarR-family regulatory protein [Streptococcus pneumoniae ATCC 700669]
Length=146

Score = 132 bits (333), Expect = 6e-30, Method: Compositional matrix adjust.
Identities = 71/143 (49%), Positives = 106/143 (74%), Gaps = 0/143 (0%)

```
Query  3    LANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKI  62
            LA  ID FL  ++  AEN+HEIL+G C S+V LT+TQEHILMLL+E+  TN+++A +L +
Sbjct  4    LAKDIDAFLNEVILQAENQHEILIGHCTSEVALTNTQEHILMLLSEESLTNSELARRLNV  63

Query  63   SPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELG  122
            S AAVTKA+K L ++ ++++S+ + D RV+ + LT+ A P+A+EH  HHE TL TY+++
Sbjct  64   SQAAVTKAIKSLVKEGMLETSKDSKDARVIFYQLTDLARPIAEEHHHHHHEHTLLTYEQVA  123

Query  123  NKFTDEEQEVISKFLSALTEEFQ  145
             +FT  EQ+VI +FL+AL  E +
Sbjct  124  TQFTPNEQKVIQRFLTALVGEIK  146
```

>**ref|NP_359569.1|** adc operon repressor AdcR [Streptococcus pneumoniae R6]
ref|ZP_01825537.1| Transcriptional repressor for Zn(2+)-responsive expression [Streptococcus pneumoniae SP11-BS70]
ref|YP_001836857.1| adc operon repressor AdcR [Streptococcus pneumoniae CGSP14]
ref|ZP_02964427.1| putative transcriptional repressor [Streptococcus pneumoniae CDC0288-04]
gb|AAL00780.1| Transcriptional repressor for Zn(2+)-responsive expression [Streptococcus pneumoniae R6]
gb|EDK63077.1| Transcriptional repressor for Zn(2+)-responsive expression [Streptococcus pneumoniae SP11-BS70]
gb|ACB91392.1| adc operon repressor AdcR [Streptococcus pneumoniae CGSP14]
gb|EDT94590.1| putative transcriptional repressor [Streptococcus pneumoniae CDC0288-04]
Length=166

GENE ID: 933868 adcR | adc operon repressor AdcR [Streptococcus pneumoniae R6]
(10 or fewer PubMed links)

Score = 131 bits (329), Expect = 2e-29, Method: Compositional matrix adjust.
Identities = 70/143 (48%), Positives = 106/143 (74%), Gaps = 0/143 (0%)

```
Query  3    LANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKI  62
```

```
            LA  I+ FL  ++  AEN+HEIL+G C S+V LT+TQEHILMLL+E+  TN+++A +L +
Sbjct  24   LAKDINAFLNEVILQAENQHEILIGHCTSEVALTNTQEHILMLLSEESLTNSELARRLNV  83

Query  63   SPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELG  122
            S AAVTKA+K L ++ ++++S+ + D RV+ + LT+ A P+A+EH  HHE TL TY+++
Sbjct  84   SQAAVTKAIKSLVKEGMLETSKDSKDARVIFYQLTDLARPIAEEHHHHHEHTLLTYEQVA  143

Query  123  NKFTDEEQEVISKFLSALTEEFQ  145
             +FT  EQ+VI +FL+AL  E +
Sbjct  144  TQFTPNEQKVIQRFLTALVGEIK  166


>ref|NP_346586.1| G adc operon repressor AdcR [Streptococcus pneumoniae TIGR4]
 ref|ZP_01408975.1| G hypothetical protein SpneT_02000553 [Streptococcus pneumoniae
TIGR4]
 ref|YP_817386.1| G adc operon repressor AdcR [Streptococcus pneumoniae D39]
 29 more sequence titles

ref|ZP_01820229.1|  adc operon repressor AdcR [Streptococcus pneumoniae SP6-BS73]
 ref|ZP_01821749.1|  adc operon repressor AdcR [Streptococcus pneumoniae SP9-BS68]
 ref|ZP_01827937.1|  adc operon repressor AdcR [Streptococcus pneumoniae SP14-BS69]
 ref|ZP_01830531.1|  adc operon repressor AdcR [Streptococcus pneumoniae SP18-BS74]
 ref|ZP_01833186.1|  adc operon repressor AdcR [Streptococcus pneumoniae SP19-BS75]
 ref|ZP_01835060.1|  adc operon repressor AdcR [Streptococcus pneumoniae SP23-BS72]
 ref|ZP_02708953.1|  putative transcriptional repressor [Streptococcus pneumoniae
CDC1873-00]
 ref|ZP_02710784.1|  putative transcriptional repressor [Streptococcus pneumoniae
CDC1087-00]
 ref|ZP_02713441.1|  putative transcriptional repressor [Streptococcus pneumoniae
SP195]
 ref|ZP_02718213.1|  putative transcriptional repressor [Streptococcus pneumoniae
CDC3059-06]
 ref|ZP_02721950.1|  putative transcriptional repressor [Streptococcus pneumoniae
MLV-016]
 ref|YP_001695528.1| G putative transcriptional repressor [Streptococcus pneumoniae
Hungary19A-6]
 ref|YP_002038763.1| G transcriptional regulator, MarR family [Streptococcus pneumoniae
G54]
 emb|CAA96184.1|  AdcR protein [Streptococcus pneumoniae]
 gb|AAK76226.1| G adc operon repressor AdcR [Streptococcus pneumoniae TIGR4]
 gb|ABJ54931.1| G adc operon repressor AdcR [Streptococcus pneumoniae D39]
 gb|EDK65765.1|  adc operon repressor AdcR [Streptococcus pneumoniae SP14-BS69]
 gb|EDK68416.1|  adc operon repressor AdcR [Streptococcus pneumoniae SP18-BS74]
 gb|EDK70926.1|  adc operon repressor AdcR [Streptococcus pneumoniae SP19-BS75]
 gb|EDK76701.1|  adc operon repressor AdcR [Streptococcus pneumoniae SP6-BS73]
 gb|EDK80035.1|  adc operon repressor AdcR [Streptococcus pneumoniae SP9-BS68]
 gb|EDK81745.1|  adc operon repressor AdcR [Streptococcus pneumoniae SP23-BS72]
 gb|ACA36761.1| G putative transcriptional repressor [Streptococcus pneumoniae
Hungary19A-6]
 gb|EDT50754.1|  putative transcriptional repressor [Streptococcus pneumoniae
CDC1873-00]
 gb|EDT91227.1|  putative transcriptional repressor [Streptococcus pneumoniae
CDC1087-00]
 gb|EDT92758.1|  putative transcriptional repressor [Streptococcus pneumoniae
SP195]
 gb|EDT96372.1|  putative transcriptional repressor [Streptococcus pneumoniae
CDC3059-06]
 gb|EDT98576.1|  putative transcriptional repressor [Streptococcus pneumoniae
MLV-016]
 gb|ACF56415.1| G transcriptional regulator, MarR family [Streptococcus pneumoniae
G54]
Length=146

 GENE ID: 931929 SP_2172 | adc operon repressor AdcR
[Streptococcus pneumoniae TIGR4] (10 or fewer PubMed links)

 Score =  130 bits (328),  Expect = 2e-29, Method: Compositional matrix adjust.
 Identities = 70/143 (48%), Positives = 106/143 (74%), Gaps = 0/143 (0%)

Query  3    LANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKI  62
            LA  I+ FL  ++  AEN+HEIL+G C S+V LT+TQEHILMLL+E+  TN+++A +L +
Sbjct  4    LAKDINAFLNEVILQAENQHEILIGHCTSEVALTNTQEHILMLLSEESLTNSELARRLNV  63

Query  63   SPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELG  122
            S AAVTKA+K L ++ ++++S+ + D RV+ + LT+ A P+A+EH  HHE TL TY+++
Sbjct  64   SQAAVTKAIKSLVKEGMLETSKDSKDARVIFYQLTDLARPIAEEHHHHHEHTLLTYEQVA  123

Query  123  NKFTDEEQEVISKFLSALTEEFQ  145
             +FT  EQ+VI +FL+AL  E +
Sbjct  124  TQFTPNEQKVIQRFLTALVGEIK  146


>ref|YP_138725.1| G zinc transport transcriptional repressor [Streptococcus thermophilus
LMG 18311]
 ref|YP_140614.1| G zinc transport transcriptional repressor [Streptococcus thermophilus
CNRZ1066]
 gb|AAV59910.1| G zinc transport transcriptional repressor [Streptococcus thermophilus
LMG 18311]
 gb|AAV61799.1| G zinc transport transcriptional repressor [Streptococcus thermophilus
CNRZ1066]
```

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Length=151

GENE ID: 3164452 adcR | zinc transport transcriptional repressor [Streptococcus thermophilus LMG 18311] (10 or fewer PubMed links)

Score = 129 bits (325), Expect = 5e-29, Method: Compositional matrix adjust.
Identities = 62/145 (42%), Positives = 104/145 (71%), Gaps = 0/145 (0%)

```
Query  1    MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL  60
            + L  Q++Q +  I+  AEN++E+L+G+C S VKLT+TQEHILMLL+E   TN+++A+ L
Sbjct  6    IELEEQVNQLINQILLKAENQYELLIGQCRSKVKLTNTQEHILMLLSEGQKTNSELAKAL  65

Query  61   KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE  120
             +S AAVTKA+K L ++ +++   +  +D RV  + LT++A P+A+EH  HH++TL  Y+
Sbjct  66   NVSQAAVTKAVKTLVKEGMLEGKKDKDDGRVTYFVLTQEAQPIAQEHKEHHQETLGVYRS  125

Query  121  LGNKFTDEEQEVISKFLSALTEEFQ  145
            + ++F  +E++VI +FL  L E+ +
Sbjct  126  VLDQFDHQERQVIGRFLIKLAEKIE  150
```

>**ref|YP_819746.1|** zinc transport transcriptional repressor [Streptococcus thermophilus LMD-9]
gb|ABJ65550.1| transcriptional regulator, MarR family [Streptococcus thermophilus LMD-9]
Length=147

GENE ID: 4438531 STER_0233 | zinc transport transcriptional repressor [Streptococcus thermophilus LMD-9] (10 or fewer PubMed links)

Score = 128 bits (322), Expect = 1e-28, Method: Compositional matrix adjust.
Identities = 61/145 (42%), Positives = 104/145 (71%), Gaps = 0/145 (0%)

```
Query  1    MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL  60
            + L  +++Q +  I+  AEN++E+L+G+C S VKLT+TQEHILMLL+E   TN+++A+ L
Sbjct  2    IELEERVNQLINQILLKAENQYELLIGQCRSKVKLTNTQEHILMLLSEGQKTNSELAKAL  61

Query  61   KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE  120
             +S AAVTKA+K L ++ +++   +  +D RV  + LT++A P+A+EH  HH++TL  Y+
Sbjct  62   NVSQAAVTKAVKTLVKEGMLEGKKDKDDGRVTYFVLTQEAQPIAQEHKEHHQETLGVYRS  121

Query  121  LGNKFTDEEQEVISKFLSALTEEFQ  145
            + ++F  +E++VI +FL  L E+ +
Sbjct  122  VLDQFDHQERQVIGRFLIKLAEKIE  146
```

>**ref|YP_001197479.1|** transcriptional regulator [Streptococcus suis 05ZYH33]
gb|ABP89079.1| Transcriptional regulator [Streptococcus suis 05ZYH33]
Length=149

GENE ID: 5099418 SSU05_0109 | transcriptional regulator [Streptococcus suis 05ZYH33] (10 or fewer PubMed links)

Score = 116 bits (290), Expect = 7e-25, Method: Compositional matrix adjust.
Identities = 70/143 (48%), Positives = 100/143 (69%), Gaps = 0/143 (0%)

```
Query  3    LANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKI  62
            +A +I+++L  I+  +EN+ EIL+G C+S VKLT+TQEHILML+ +   TN +IA++L +
Sbjct  6    IALEIEKYLHEIVLSSENQLEILVGSCQSTVKLTNTQEHILMLIEKAAYTNTEIAKELNV  65

Query  63   SPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELG  122
            S AA+TKA K L  Q L+ + R   D R+V +SLTE A P+A EHA HH  TL  Y+EL
Sbjct  66   SQAAITKATKSLVAQGLLVAVRDDKDARIVRFSLTEAAKPIAAEHAHHHAHTLEAYEELL  125

Query  123  NKFTDEEQEVISKFLSALTEEFQ  145
              ++ EEQE I++FLS L E+ +
Sbjct  126  ENYSLEEQESIARFLSELVEKIR  148
```

>**ref|ZP_03625066.1|** transcriptional regulator, MarR family [Streptococcus suis 89/1591]
gb|EEF64628.1| transcriptional regulator, MarR family [Streptococcus suis 89/1591]
Length=149

Score = 110 bits (275), Expect = 4e-23, Method: Compositional matrix adjust.
Identities = 69/140 (49%), Positives = 98/140 (70%), Gaps = 0/140 (0%)

```
Query  6    QIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKISPA  65
            +I+++L  I+  +EN+ EIL+G C+S VKLT+TQEHILML+ +   TN +IA++L +S A
Sbjct  9    EIEKYLHEIVLSSENQLEILVGSCQSTVKLTNTQEHILMLIEKAAYTNTEIAKELNVSQA  68

Query  66   AVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKF  125
            A+TKA K L  Q L+ + R   D R+V +SLTE A P+A EHA HH  TL  Y+EL   +
Sbjct  69   AITKATKSLVAQGLLVAVRDDKDARIVRFSLTEAAKPIATEHAHHHAHTLEAYEELLEHY  128

Query  126  TDEEQEVISKFLSALTEEFQ  145
            + EEQE I++FLS L E+ +
Sbjct  129  SLEEQESIARFLSELVEKIR  148
```

>**emb|CAA75313.1|** hypothetical protein [Lactococcus lactis subsp. cremoris]
Length=48

Score = 92.4 bits (228), Expect = 1e-17, Method: Compositional matrix adjust.
Identities = 43/47 (91%), Positives = 46/47 (97%), Gaps = 0/47 (0%)

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```
Query  1    MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLA  47
            MSLANQIDQFLG IMQFAENKHEILLG+CES+VKLTSTQEHILM+LA
Sbjct  1    MSLANQIDQFLGAIMQFAENKHEILLGECESNVKLTSTQEHILMILA  47
```

>ref|ZP_00365496.1| COG1846: Transcriptional regulators [Streptococcus pyogenes M49 591]
Length=103

```
 Score = 90.9 bits (224),  Expect = 3e-17, Method: Compositional matrix adjust.
 Identities = 45/102 (44%), Positives = 68/102 (66%), Gaps = 0/102 (0%)

Query  44   MLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPV  103
            MLL++Q  TN  +A+ L IS AAVTKA+K L +Q+++  ++ T D RV  + LTE A P+
Sbjct  1    MLLSQQRLTNTDLAKALNISQAAVTKAIKSLVKQDMLAGTKDTVDARVTYFELTELAKPI  60

Query  104  AKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEFQ  145
            A EH  HH++TL+ Y  L  KF+ +E E++ KF++   EE +
Sbjct  61   ASEHTHHHDETLNVYNRLLQKFSAKELEIVDKFVTVFAEELE  102
```

>ref|YP_001485459.1| G MarR family transcriptional regulator [Bacillus pumilus SAFR-032]
ref|ZP_03056081.1| YvnA [Bacillus pumilus ATCC 7061]
gb|ABV60899.1| G possible MarR family transcriptional regulator [Bacillus pumilus SAFR-032]
gb|EDW20313.1| YvnA [Bacillus pumilus ATCC 7061]
Length=152

GENE ID: 5619427 BPUM_0200 | MarR family transcriptional regulator [Bacillus pumilus SAFR-032] (10 or fewer PubMed links)

```
 Score = 67.0 bits (162),  Expect = 5e-10, Method: Compositional matrix adjust.
 Identities = 40/111 (36%), Positives = 66/111 (59%), Gaps = 2/111 (1%)

Query  36   TSTQEHILMLLAEQI--STNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVL  93
            T TQ HIL ++       S N  ++++LK+S  A+TKA+KKL ++ ++       D++ V
Sbjct  42   TLTQLHILSMIQANPNESNNTFLSQQLKLSKPAITKAVKKLIDKGMVDYCHRQGDKKSVY  101

Query  94   WSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF  144
            +SLTEK   +A  H   HEK +++Y E   +F ++E +VI +FL A  E+
Sbjct  102  YSLTEKGTQLAALHDELHEKAVASYLEFLQQFHEDELQVIERFLKAWKEKI  152
```

>ref|YP_001199672.1| G transcriptional regulator [Streptococcus suis 98HAH33]
gb|ABP91272.1| G Transcriptional regulator [Streptococcus suis 98HAH33]
Length=87

GENE ID: 5101832 SSU98_0112 | transcriptional regulator [Streptococcus suis 98HAH33] (10 or fewer PubMed links)

```
 Score = 63.2 bits (152),  Expect = 6e-09, Method: Compositional matrix adjust.
 Identities = 41/86 (47%), Positives = 56/86 (65%), Gaps = 0/86 (0%)

Query  60   LKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQ  119
            + +S AA+TKA K L  Q L+ + R   D R+V +SLTE A P+A EHA HH  TL  Y+
Sbjct  1    MNVSQAAITKATKSLVAQGLLVAVRDDKDARIVRFSLTEAAKPIAAEHAHHHAHTLEAYE  60

Query  120  ELGNKFTDEEQEVISKFLSALTEEFQ  145
            EL   ++ EEQE I++FLS L E+ +
Sbjct  61   ELLENYSLEEQESIARFLSELVEKIR  86
```

>ref|YP_187318.1| G MarR family transcriptional regulator [Staphylococcus aureus subsp. aureus COL]
ref|YP_495086.1| G MarR family transcriptional regulator [Staphylococcus aureus subsp. aureus USA300]
ref|YP_001576367.1| G MarR family transcriptional regulator [Staphylococcus aureus subsp. aureus USA300_TCH1516]
ref|ZP_02761767.1| G MarR family transcriptional regulator [Staphylococcus aureus subsp. aureus USA300_TCH1516]
gb|AAW37302.1| G transcriptional regulator, MarR family [Staphylococcus aureus subsp. aureus COL]
gb|ABD21126.1| G transcriptional regulator, MarR family [Staphylococcus aureus subsp. aureus USA300_FPR3757]
gb|ABX30488.1| G MarR family transcriptional regulator [Staphylococcus aureus subsp. aureus USA300_TCH1516]
Length=154

GENE ID: 3238188 SACOL2524 | MarR family transcriptional regulator [Staphylococcus aureus subsp. aureus COL] (10 or fewer PubMed links)

```
 Score = 63.2 bits (152),  Expect = 7e-09, Method: Compositional matrix adjust.
 Identities = 40/112 (35%), Positives = 66/112 (58%), Gaps = 1/112 (0%)

Query  35   LTSTQEHILMLLAEQISTNAK-IAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVL  93
            L+ TQ HI+ L+       N K ++E L +S  A+TK++KKL  ++L+  S    ++R V
Sbjct  36   LSLTQFHIIELIDNNDKVNNKFLSEMLNVSKPAITKSIKKLLAKDLVVESHNEFNKREVN  95

Query  94   WSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEFQ  145
            +SLT+K   ++   H   HEK++  Y+E+   F D+E  VI +FL+   EE +
Sbjct  96   YSLTQKGKKLSYIHDELHEKSVKKYEEVLKVFDDDEMAVIIEFLNRSIEELK  147
```

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>**ref|YP_001727325.1|** transcriptional repressor for Zn(2+)-responsive expression [Leuconostoc citreum KM20]
gb|ACA81881.1| Transcriptional repressor for Zn(2+)-responsive expression [Leuconostoc citreum KM20]
Length=146

GENE ID: 6063203 adcR | transcriptional repressor for Zn(2+)-responsive expression [Leuconostoc citreum KM20] (10 or fewer PubMed links)

Score = 62.8 bits (151), Expect = 8e-09, Method: Compositional matrix adjust.
Identities = 41/138 (29%), Positives = 72/138 (52%), Gaps = 2/138 (1%)

```
Query  1    MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL  60
            MS ++ I Q L T +Q      E +  +  +  K+ +TQ H+LMLL  Q +TN+ +AE +
Sbjct  1    MSQSDHIIQELNTFVQTYAASSEFI--QTTAAQKINATQAHLLMLLKTQHATNSSLAESM  58

Query  61   KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE  120
             ++  A+TKA+K L     + +++  ND+R V + L+ + + +A +H    H
Sbjct  59   HLTKPAITKAIKNLIAHGYVVATKDVNDKRSVNYQLSTEGMQLAAQHEASHRNLHHRIDH  118

Query  121  LGNKFTDEEQEVISKFLS  138
             FT  ++E I  FL+
Sbjct  119  TIATFTPAQRETIVAFLA  136
```

>**ref|YP_501277.1|** hypothetical protein SAOUHSC_02819 [Staphylococcus aureus subsp. aureus NCTC 8325]
ref|YP_001333445.1| transcriptional regulator MarR family protein [Staphylococcus aureus subsp. aureus str. Newman]
gb|ABD31821.1| conserved hypothetical protein [Staphylococcus aureus subsp. aureus NCTC 8325]
dbj|BAF68683.1| transcriptional regulator MarR family protein [Staphylococcus aureus subsp. aureus str. Newman]
Length=152

GENE ID: 3921258 SAOUHSC_02819 | hypothetical protein [Staphylococcus aureus subsp. aureus NCTC 8325]

Score = 62.8 bits (151), Expect = 8e-09, Method: Compositional matrix adjust.
Identities = 40/112 (35%), Positives = 66/112 (58%), Gaps = 1/112 (0%)

```
Query  35   LTSTQEHILMLLAEQISTNAK-IAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVL  93
            L+ TQ HI+ L+      N K ++E L +S  A+TK++KKL  ++L+  S    ++R V
Sbjct  34   LSLTQFHIIELIDNNDKVNNKFLSEMLNVSKPAITKSIKKLLAKDLVVESHNEFNKREVN  93

Query  94   WSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEFQ  145
            +SLT+K   ++  H   HEK++  Y+E+   F D+E  VI +FL+   EE +
Sbjct  94   YSLTQKGKKLSYIHDELHEKSVKKYEEVLKVFDDDEMAVIIEFLNRSIEELK  145
```

>**ref|ZP_03563431.1|** MarR family transcriptional regulator [Staphylococcus aureus subsp. aureus str. JKD6008]
ref|ZP_03566444.1| MarR family transcriptional regulator [Staphylococcus aureus subsp. aureus str. JKD6009]
Length=154

Score = 61.2 bits (147), Expect = 3e-08, Method: Compositional matrix adjust.
Identities = 40/112 (35%), Positives = 65/112 (58%), Gaps = 1/112 (0%)

```
Query  35   LTSTQEHILMLLAEQISTNAK-IAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVL  93
            L+ TQ HI+ L+      N K ++E L +S  A+TK++KKL  ++L+  S    ++R V
Sbjct  36   LSLTQFHIIELIDNNDKVNNKFLSEMLNVSKPAITKSIKKLLAKDLVVESHNEFNKREVN  95

Query  94   WSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEFQ  145
             SLT+K   ++  H   HEK++  Y+E+   F D+E  VI +FL+   EE +
Sbjct  96   CSLTQKGKKLSYIHDELHEKSVKKYEEVLKVFDDDEMAVIIEFLNRSIEELK  147
```

>**ref|YP_174450.1|** MarR family transcriptional regulator [Bacillus clausii KSM-K16]
dbj|BAD63489.1| MarR family transcriptional regulator [Bacillus clausii KSM-K16]
Length=153

GENE ID: 3204362 ABC0950 | MarR family transcriptional regulator [Bacillus clausii KSM-K16] (10 or fewer PubMed links)

Score = 60.5 bits (145), Expect = 4e-08, Method: Compositional matrix adjust.
Identities = 40/128 (31%), Positives = 73/128 (57%), Gaps = 3/128 (2%)

```
Query  18   AENKHEILLGKCESDV--KLTSTQEHILMLLAEQ-ISTNAKIAEKLKISPAAVTKALKKL  74
            A+ + + + G  E  +    T TQ HI+ ++ EQ  + N  +AE L +S  A+TKA+KKL
Sbjct  21   ADRRRKAMKGSQEESIVSDWTLTQLHIVAIVKEQERANNTMLAEHLNVSKPAITKAVKKL  80

Query  75   QEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVIS  134
             +Q+++ ++  +++ V + LT+    +A  H+  HE+  + Y  +  +F   E E I
Sbjct  81   LDQQILEKTQQADNKKEVYYRLTKSGEMLAFIHSQLHEQARNRYMRIFAEFNSTELETII  140

Query  135  KFLSALTE  142
            +FL AL E
Sbjct  141  RFLHALAE  148
```

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>ref|YP_080661.1| transcriptional regulator YvnA [Bacillus licheniformis ATCC 14580]
gb|AAU25023.1| probable transcriptional regulator YvnA [Bacillus licheniformis ATCC 14580]
Length=157

GENE ID: 3028745 yvnA | transcriptional regulator YvnA [Bacillus licheniformis ATCC 14580] (10 or fewer PubMed links)

Score = 59.3 bits (142), Expect = 1e-07, Method: Compositional matrix adjust.
Identities = 37/105 (35%), Positives = 64/105 (60%), Gaps = 2/105 (1%)

```
Query  36   TSTQEHILMLLAEQIS--TNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVL  93
            T TQ HI+ L++E  +   NA +A KL+IS AAVTKA+  L +  +I+S +  N+ + +
Sbjct  47   TLTQLHIISLISESEADVNNAFLAAKLQISKAAVTKAVNVLTKHGMIESHKKPNNNKELY  106

Query  94   WSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLS  138
            ++LT++   +A  H   HE     Y EL ++F++ E + + +FL+
Sbjct  107  YTLTDEGKKLADIHDRMHEIAKQRYIELFDRFSESELQTVIRFLN  151
```

>ref|YP_254603.1| hypothetical protein pSHaeC05 [Staphylococcus haemolyticus JCSC1435]
dbj|BAE05997.1| unnamed protein product [Staphylococcus haemolyticus JCSC1435]
Length=155

GENE ID: 3431756 pSHaeC05 | hypothetical protein [Staphylococcus haemolyticus JCSC1435] (10 or fewer PubMed links)

Score = 59.3 bits (142), Expect = 1e-07, Method: Compositional matrix adjust.
Identities = 38/119 (31%), Positives = 69/119 (57%), Gaps = 1/119 (0%)

```
Query  28   KCESDVKLTSTQEHILMLLAEQISTNAK-IAEKLKISPAAVTKALKKLQEQELIKSSRAT  86
            K   D+ L+ TQ HI+ ++ +    N K +AE+L +S  AVTK++KKL  +EL+
Sbjct  29   KGNEDMDLSLTQFHIIEIIDKHEKVNNKFLAEELNVSKPAVTKSIKKLLSKELVVELNNE  88

Query  87   NDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEFQ  145
            +++R V ++LT++   ++  H   H+K +  Y+E+   F ++E E I +FL    +E +
Sbjct  89   SNKREVYYNLTKRGEKLSFIHDDLHKKAVKKYEEVLKVFDEKEMETIIEFLKRSVDELK  147
```

>ref|YP_093087.1| YvnA [Bacillus licheniformis ATCC 14580]
gb|AAU42394.1| YvnA [Bacillus licheniformis DSM 13]
Length=160

GENE ID: 3100261 yvnA | similar to proteins from B. subtilis [Bacillus licheniformis ATCC 14580] (10 or fewer PubMed links)

Score = 59.3 bits (142), Expect = 1e-07, Method: Compositional matrix adjust.
Identities = 37/105 (35%), Positives = 64/105 (60%), Gaps = 2/105 (1%)

```
Query  36   TSTQEHILMLLAEQIS--TNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVL  93
            T TQ HI+ L++E  +   NA +A KL+IS AAVTKA+  L +  +I+S +  N+ + +
Sbjct  50   TLTQLHIISLISESEADVNNAFLAAKLQISKAAVTKAVNVLTKHGMIESHKKPNNNKELY  109

Query  94   WSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLS  138
            ++LT++   +A  H   HE     Y EL ++F++ E + + +FL+
Sbjct  110  YTLTDEGKKLADIHDRMHEIAKQRYIELFDRFSESELQTVIRFLN  154
```

>ref|ZP_00738634.1| Transcriptional regulator, MarR family [Bacillus thuringiensis serovar israelensis ATCC 35646]
gb|EAO57135.1| Transcriptional regulator, MarR family [Bacillus thuringiensis serovar israelensis ATCC 35646]
Length=156

Score = 55.8 bits (133), Expect = 9e-07, Method: Compositional matrix adjust.
Identities = 32/106 (30%), Positives = 64/106 (60%), Gaps = 2/106 (1%)

```
Query  36   TSTQEHILMLLAE--QISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVL  93
            T TQ HI+ ++ E  Q    N  ++ +L IS A ++KA++ L + +++ + + T++++ +
Sbjct  46   TLTQLHIVSVIHESKQQMNNTLLSMELNISKATISKAIRVLIDNKILLTHQNTDNKKEIF  105

Query  94   WSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSA  139
            ++LT+K + +A  H   H+     Y EL  +F D E ++++KFL A
Sbjct  106  YTLTDKGIQLAIVHKKLHKIAHERYSELFQQFNDSELQIVTKFLEA  151
```

>ref|ZP_02613091.1| transcriptional regulator, MarR family [Clostridium botulinum NCTC 2916]
gb|EDT83321.1| transcriptional regulator, MarR family [Clostridium botulinum NCTC 2916]
Length=174

Score = 54.3 bits (129), Expect = 3e-06, Method: Compositional matrix adjust.
Identities = 35/113 (30%), Positives = 62/113 (54%), Gaps = 2/113 (1%)

```
Query  30   ESDVKLTSTQE-HILMLLAEQ-ISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATN  87
            ++D+K  S  E H++  + +  +S N  IA +L ++   ++K  KL  +++IK+ +  N
Sbjct  58   DNDIKGISLSEFHVIECIGKNNMSNNIFIARELNMTKGGISKINSKLLSKDIIKADKIEN  117

Query  88   DERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSAL  140
            D+R + +SLTEK + + K H   HEK      ++ + +  EE   I KFL  L
Sbjct  118  DKREIYYSLTEKGIALFKLHEYLHEKEREKLMKILSNYKLEEITTILKFLEDL  170
```

Annex 1

>**ref|YP_001253547.1|** MarR family transcriptional regulator [Clostridium botulinum A str. ATCC 3502]
ref|YP_001383390.1| MarR family transcriptional regulator [Clostridium botulinum A str. ATCC 19397]
ref|YP_001386937.1| MarR family transcriptional regulator [Clostridium botulinum A str. Hall]
emb|CAL82569.1| MarR-family transcriptional regulator [Clostridium botulinum A str. ATCC 3502]
gb|ABS35317.1| transcriptional regulator, MarR family [Clostridium botulinum A str. ATCC 19397]
gb|ABS36227.1| transcriptional regulator, MarR family [Clostridium botulinum A str. Hall]
Length=174

GENE ID: 5185271 CBO1016 | MarR family transcriptional regulator [Clostridium botulinum A str. ATCC 3502] (10 or fewer PubMed links)

Score = 54.3 bits (129), Expect = 3e-06, Method: Compositional matrix adjust.
Identities = 35/113 (30%), Positives = 63/113 (55%), Gaps = 2/113 (1%)

```
Query  30   ESDVKLTSTQE-HILMLLAEQ-ISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATN  87
            ++D+K  S  E H++  + +  +S N  IA++L ++   ++K   KL  +++IK+ +  N
Sbjct  58   DNDIKGISLSEFHVIECIGKNNMSNNIFIAKELNMTKGGISKINSKLLSKDIIKADKIEN  117

Query  88   DERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSAL  140
            D+R + +SLTEK + + K H    HEK      ++ + +  EE   I KFL  L
Sbjct  118  DKREIYYSLTEKGIALFKLHEHLHEKEREKLMKILSNYKLEEITTILKFLEDL  170
```

>**ref|YP_001780642.1|** MarR family transcriptional regulator [Clostridium botulinum B1 str. Okra]
gb|ACA44681.1| transcriptional regulator, MarR family [Clostridium botulinum B1 str. Okra]
Length=174

GENE ID: 6149223 CLD_3550 | MarR family transcriptional regulator [Clostridium botulinum B1 str. Okra] (10 or fewer PubMed links)

Score = 54.3 bits (129), Expect = 3e-06, Method: Compositional matrix adjust.
Identities = 35/113 (30%), Positives = 63/113 (55%), Gaps = 2/113 (1%)

```
Query  30   ESDVKLTSTQE-HILMLLAEQ-ISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATN  87
            ++D+K  S  E H++  + +  +S N  IA++L ++   ++K   KL  +++IK+ +  N
Sbjct  58   DNDIKGISLSEFHVIECIGKNNMSNNIFIAKELNMTKGGISKINSKLLSKDIIKADKIEN  117

Query  88   DERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSAL  140
            D+R + +SLTEK + + K H    HEK      ++ + +  EE   I KFL  L
Sbjct  118  DKREIYYSLTEKGIALFKLHEHLHEKEREKLMKILSNYKLEEITTILKFLEDL  170
```

>**ref|YP_001033131.1|** MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]
emb|CAL98430.1| transcriptional regulator, MarR family [Lactococcus lactis subsp. cremoris MG1363]
Length=295

GENE ID: 4797387 rmaB | MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 53.9 bits (128), Expect = 4e-06, Method: Compositional matrix adjust.
Identities = 38/101 (37%), Positives = 54/101 (53%), Gaps = 3/101 (2%)

```
Query  42   ILMLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAV  101
            ++ L  E   TNA+IAE L I P++VT  +K+L+E E++   +  ND+RV    LTEK
Sbjct  47   LVELWNEDGLTNAEIAELLDIKPSSVTTQVKQLEEAEMVIRKQDENDKRVNRIFLTEKGR  106

Query  102  PVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTE  142
               +   T H     T    GN  TDEEQE ++  +  L E
Sbjct  107  EAQETRDTMHNDISETI--FGN-LTDEEQEQLANLMEKLVE  144
```

>**ref|ZP_02617530.1|** transcriptional regulator, MarR family [Clostridium botulinum Bf]
gb|EDT85893.1| transcriptional regulator, MarR family [Clostridium botulinum Bf]
Length=174

Score = 53.9 bits (128), Expect = 4e-06, Method: Compositional matrix adjust.
Identities = 35/113 (30%), Positives = 62/113 (54%), Gaps = 2/113 (1%)

```
Query  30   ESDVKLTSTQE-HILMLLAEQ-ISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATN  87
            ++D+K  S  E H++  + +  +S N  IA+ L ++   ++K   KL  +++IK+ +  N
Sbjct  58   DNDIKGISLSEFHVIECIGKNNMSNNIFIAKDLNMTKGGISKINSKLLSKDIIKADKIEN  117

Query  88   DERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSAL  140
            D+R + +SLTEK + + K H    HEK      ++ + +  EE   I KFL  L
Sbjct  118  DKREIYYSLTEKGIALFKLHEHIHEKEREKLMKILSNYKLEEITTILKFLEDL  170
```

>**ref|YP_861960.1|** MarR family transcriptional regulator [Gramella forsetii KT0803]
emb|CAL66893.1| MarR family transcriptional regulator protein [Gramella forsetii

KT0803]
Length=158

GENE ID: 4650237 GFO_1928 | MarR family transcriptional regulator [Gramella forsetii KT0803] (10 or fewer PubMed links)

Score = 53.9 bits (128), Expect = 4e-06, Method: Compositional matrix adjust.
Identities = 39/112 (34%), Positives = 65/112 (58%), Gaps = 8/112 (7%)

```
Query  1    MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQ--ISTNAKIAE  58
            + L NQI    + ++ +      ++  L K E     LT  Q  +L++L E+  +S N KI E
Sbjct  7    LKLENQICFPIYSVSRLITKAYKPYLDKLE----LTYPQYLVLLVLWEEHKLSVN-KIGE  61

Query  59   KLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATH  110
            KL ++    ++  LK++++ EL+K +R++NDER VL  LT+K +   KE A H
Sbjct  62   KLMLNTNTLSPLLKRMEKNELLKRNRSSNDERTVLVGLTDKGLSY-KEKAAH  112
```

>**ref|NP_391388.1|** hypothetical protein BSU35080 [Bacillus subtilis subsp. subtilis str. 168]
ref|ZP_03593305.1| hypothetical protein Bsubs1_18986 [Bacillus subtilis subsp. subtilis str. 168]
ref|ZP_03597590.1| hypothetical protein BsubsN3_18902 [Bacillus subtilis subsp. subtilis str. NCIB 3610]
6 more sequence titles

ref|ZP_03601994.1| hypothetical protein BsubsJ_18865 [Bacillus subtilis subsp. subtilis str. JH642]
ref|ZP_03606279.1| hypothetical protein BsubsS_19021 [Bacillus subtilis subsp. subtilis str. SMY]
sp|P40762.1|YVMB_BACSU RecName: Full=Uncharacterized HTH-type transcriptional regulator yvmB
emb|CAA85355.1| unnamed protein product [Bacillus subtilis]
gb|AAC67278.1| YzhA [Bacillus subtilis]
emb|CAB15513.1| yvmB [Bacillus subtilis subsp. subtilis str. 168]
Length=169

GENE ID: 936625 yvmB | yvmB [Bacillus subtilis subsp. subtilis str. 168] (10 or fewer PubMed links)

Score = 53.5 bits (127), Expect = 5e-06, Method: Compositional matrix adjust.
Identities = 36/91 (39%), Positives = 53/91 (58%), Gaps = 2/91 (2%)

```
Query  52   TNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEH-ATH  110
             NA IA K+ +S A VTK   KL ++E I S + T++++ V + LT K   +   H   H
Sbjct  63   NNAGIARKMNLSKANVTKISTKLIKEEFINSYQLTDNKKEVYFKLTRKGRRIFDLHEKLH  122

Query  111  HEKTLSTYQELGNKFTDEEQEVISKFLSALT  141
             +K L+ YQ L + F+ EEQ+ + KFL  LT
Sbjct  123  KKKELAFYQFL-DSFSQEEQKAVLKFLEQLT  152
```

>**ref|ZP_02994615.1|** hypothetical protein CLOSPO_01734 [Clostridium sporogenes ATCC 15579]
gb|EDU38872.1| hypothetical protein CLOSPO_01734 [Clostridium sporogenes ATCC 15579]
Length=174

Score = 53.5 bits (127), Expect = 6e-06, Method: Compositional matrix adjust.
Identities = 34/113 (30%), Positives = 63/113 (55%), Gaps = 2/113 (1%)

```
Query  30   ESDVKLTSTQE-HILMLLAEQ-ISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATN  87
            ++D+K  S  E H++  + +  +S N  IA++L ++   ++K   KL  +++IK+ +  N
Sbjct  58   DNDIKEISLSEFHVIECIGKNNMSNNIFIAKELNMTKGGISKINSKLLSKDIIKADKIEN  117

Query  88   DERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSAL  140
            D+R + +SLTEK + + K H   H+K      ++ + +  EE   I KFL  L
Sbjct  118  DKREIYYSLTEKGIVLFKLHEYLHKKEQEKLMKILSNYKQEEITTILKFLDDL  170
```

>**ref|ZP_01994138.1|** hypothetical protein DORLON_00120 [Dorea longicatena DSM 13814]
gb|EDM64274.1| hypothetical protein DORLON_00120 [Dorea longicatena DSM 13814]
Length=153

Score = 53.1 bits (126), Expect = 6e-06, Method: Compositional matrix adjust.
Identities = 36/111 (32%), Positives = 55/111 (49%), Gaps = 4/111 (3%)

```
Query  35   LTSTQEHILMLLAEQISTN-AKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVL  93
            LT+   H++  +      N + IA KL I+  ++T A+  L  +  ++  R+  D RVVL
Sbjct  37   LTNNDMHVIEAVGLGDGNNMSSIARKLNITVGSLTTAMNSLVNKRYVERHRSEEDRRVVL  96

Query  94   WSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF  144
              LTEK V     H  +H +     Q + +K  D E  V+ K L AL+E F
Sbjct  97   VKLTEKGVKAYHHHEDYHRQMT---QAILDKLDDTELPVLVKTLDALSEFF  144
```

>**ref|ZP_03294064.1|** hypothetical protein CLOHIR_02015 [Clostridium hiranonis DSM 13275]
gb|EEA84316.1| hypothetical protein CLOHIR_02015 [Clostridium hiranonis DSM 13275]
Length=166

Score = 53.1 bits (126), Expect = 7e-06, Method: Compositional matrix adjust.
Identities = 37/131 (28%), Positives = 68/131 (51%), Gaps = 6/131 (4%)

```
Query  13   TIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTN-AKIAEKLKISPAAVTKAL  71
```

```
            T  +F    HE   G+     K+   + H++  + E    N ++++E+L I+  AV++ L
Sbjct  20   TYYKFLSTPHEYYPGE-----KMHMREVHVITEIGEGGLDNISELSERLNITKGAVSQYL  74

Query  72   KKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQE  131
            KKL+++  I+  + + D+R     LTEK   + K H  + E+  +      N+FT+EE E
Sbjct  75   KKLEKKGFIERVQESEDKRQYSVRLTEKGKELDKIHTKYDEEQYAKACPFFNEFTEEELE  134

Query  132  VISKFLSALTE  142
            +I +F +   E
Sbjct  135  LICRFEARFAE  145
```

>**ref|ZP_02211326.1|** hypothetical protein CLOBAR_00939 [Clostridium bartlettii DSM 16795]
gb|EDQ97187.1| hypothetical protein CLOBAR_00939 [Clostridium bartlettii DSM 16795]
Length=150

```
 Score = 52.4 bits (124),  Expect = 1e-05, Method: Compositional matrix adjust.
 Identities = 33/94 (35%), Positives = 50/94 (53%), Gaps = 3/94 (3%)

Query  52   TNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHH  111
            T  +IA  L+I+   +T A+ +L ++   + SR   D RVVL SLTEK     K HA  H
Sbjct  53   TMGEIAHDLRITVGTLTSAINRLIKKGYAERSRTEEDRRVVLVSLTEKGKHAYKIHADFH  112

Query  112  EKTLSTYQELGNKFTDEEQEVISKFLSALTEEFQ  145
            ++ +   Q   N + DEEQEV+   +  +   F+
Sbjct  113  KEMV---QATLNSYNDEEQEVLCDVIEKINIFFE  143
```

>**ref|YP_001390364.1|** MarR family transcriptional regulator [Clostridium botulinum F str. Langeland]
gb|ABS39442.1| transcriptional regulator, MarR family [Clostridium botulinum F str. Langeland]
Length=174

GENE ID: 5405444 CLI_1098 | MarR family transcriptional regulator [Clostridium botulinum F str. Langeland]

```
 Score = 52.4 bits (124),  Expect = 1e-05, Method: Compositional matrix adjust.
 Identities = 34/113 (30%), Positives = 62/113 (54%), Gaps = 2/113 (1%)

Query  30   ESDVKLTSTQE-HILMLLAEQ-ISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATN  87
            ++D+K  S  E H++  + +  +S N  IA++L ++   ++K   KL  +++IK+ +  N
Sbjct  58   DNDIKGISLSEFHVIECIGKNNMSNNIFIAKELNMTKGGISKINSKLLSKDIIKADKIEN  117

Query  88   DERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSAL  140
            D+R + +SLTEK + + K H   HEK      ++ + +  EE   I  FL  L
Sbjct  118  DKREIYYSLTEKGIALFKLHEHLHEKEREKLMKILSNYKLEEITTILNFLEDL  170
```

>**ref|YP_001786407.1|** MarR family transcriptional regulator [Clostridium botulinum A3 str. Loch Maree]
gb|ACA55750.1| transcriptional regulator, MarR family [Clostridium botulinum A3 str. Loch Maree]
Length=174

GENE ID: 6154364 CLK_0459 | MarR family transcriptional regulator [Clostridium botulinum A3 str. Loch Maree] (10 or fewer PubMed links)

```
 Score = 51.6 bits (122),  Expect = 2e-05, Method: Compositional matrix adjust.
 Identities = 33/113 (29%), Positives = 62/113 (54%), Gaps = 2/113 (1%)

Query  30   ESDVKLTSTQE-HILMLLAEQ-ISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATN  87
            ++D+K  S  E H++  + +  +  N  IA++L ++   ++K   KL  +++IK+ +  N
Sbjct  58   DNDIKGISLSEFHVIECIGKNNMPNNIFIAKELNMTKGGISKINSKLLLKDIIRADKIEN  117

Query  88   DERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSAL  140
            D+R + +SLTEK + + K H   HEK      ++ + +  EE   I KFL  L
Sbjct  118  DKREIYYSLTEKGIALFKLHEHLHEKEREKLMKILSNYKQEEITTILKFLEDL  170
```

>**ref|YP_808725.1|** transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
gb|ABJ72303.1| Transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
Length=292

GENE ID: 4432217 LACR_0742 | transcriptional regulator [Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

```
 Score = 51.2 bits (121),  Expect = 2e-05, Method: Compositional matrix adjust.
 Identities = 35/91 (38%), Positives = 50/91 (54%), Gaps = 3/91 (3%)

Query  52   TNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHH  111
            TNA+IAE L I P++VT  +K+L+E E++   +  ND+RV    LTEK     +  T H
Sbjct  57   TNAEIAELLDIKPSSVTAQVKQLEEAEMVIRKQDENDKRVNRIFLTEKGREAQETRDTMH  116

Query  112  EKTLSTYQELGNKFTDEEQEVISKFLSALTE  142
                 T    GN  TDEEQ+ ++  +  L E
Sbjct  117  NDISETI--FGN-LTDEEQKQLANLMEKLVE  144
```

>ref|YP_001698248.1| MarR family transcriptional regulator [Lysinibacillus sphaericus C3-41]
gb|ACA40118.1| transcriptional regulator, MarR family [Lysinibacillus sphaericus C3-41]
Length=162

GENE ID: 6022244 Bsph_2567 | MarR family transcriptional regulator [Lysinibacillus sphaericus C3-41] (10 or fewer PubMed links)

Score = 51.2 bits (121), Expect = 3e-05, Method: Compositional matrix adjust.
Identities = 36/111 (32%), Positives = 60/111 (54%), Gaps = 1/111 (0%)

```
Query  36   TSTQEHILMLLAEQISTNAK-IAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLW  94
            T TQ HI+  +  Q S N   ++E L +S  A+TKA+KK+ E+ +I  +R   +++ V +
Sbjct  44   TLTQLHIVSAIKAQGSANNTFLSETLNVSKPAITKAIKKMLEKNVIVETRQEANQKEVHY  103

Query  95   SLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEFQ  145
              LT     ++  H   HEK  + Y  L + F  +E E I  FL  +T++ +
Sbjct  104  LLTAFGKQLSSIHEQLHEKARNRYLRLLDSFNTDELETIVTFLEMITDKLK  154
```

>ref|NP_266864.1| transcription regulator [Lactococcus lactis subsp. lactis Il1403]
gb|AAK04806.1|AE006304_6 transcriptional regulator [Lactococcus lactis subsp. lactis Il1403]
Length=291

GENE ID: 1114333 rmaB | transcription regulator [Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 51.2 bits (121), Expect = 3e-05, Method: Compositional matrix adjust.
Identities = 35/91 (38%), Positives = 50/91 (54%), Gaps = 3/91 (3%)

```
Query  52   TNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHH  111
            TNA+IAE L I P++VT  +K+L+E E++   +  ND+RV    LT+K     +   T H
Sbjct  57   TNAEIAELLDIKPSSVTAQVKQLEEAEMVIRKQDENDKRVSRIFLTDKGREAQETRDTMH  116

Query  112  EKTLSTYQELGNKFTDEEQEVISKFLSALTE  142
                 T    GN  TDEEQE ++  +  L E
Sbjct  117  NDISETI--FGN-LTDEEQEQLAFLMEKLVE  144
```

>ref|ZP_01723095.1| transcriptional regulator, MarR family protein [Bacillus sp. B14905]
gb|EAZ86562.1| transcriptional regulator, MarR family protein [Bacillus sp. B14905]
Length=162

Score = 50.4 bits (119), Expect = 4e-05, Method: Compositional matrix adjust.
Identities = 35/111 (31%), Positives = 60/111 (54%), Gaps = 1/111 (0%)

```
Query  36   TSTQEHILMLLAEQISTNAK-IAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLW  94
            T TQ HI+  +  Q S N   ++E L +S  A+TKA+KK+ E+ +I  +R   +++ + +
Sbjct  44   TLTQLHIVSAIKAQGSANNTFLSETLNVSKPAITKAIKKMLEKNVIVETRQEANQKEIHY  103

Query  95   SLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEFQ  145
              LT     ++  H   HEK  + Y  L + F  +E E I  FL  +T++ +
Sbjct  104  LLTAFGKQLSSIHEQLHEKARNRYLRLLDSFNTDELETIITFLEMITDKLK  154
```

>ref|YP_808147.1| transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
gb|ABJ71725.1| Transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
Length=169

GENE ID: 4432499 LACR_0099 | transcriptional regulator [Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 50.4 bits (119), Expect = 5e-05, Method: Compositional matrix adjust.
Identities = 27/98 (27%), Positives = 55/98 (56%), Gaps = 0/98 (0%)

```
Query  41   HILMLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKA  100
            HIL  L ++  T  ++A KL ++   VT+A++ L + + + + +A ND++ + + +T K
Sbjct  53   HILSALTKKDLTGIELATKLSVTRGGVTRAVQNLIKHQFLTTYQADNDKKKIYYHITTKG  112

Query  101  VPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLS  138
            + VA  H   H+          ++ +K+ + E+ +I  FLS
Sbjct  113  LKVASIHDKMHKIMDLKLGQIFDKYNENEKSIILNFLS  150
```

>ref|NP_786298.1| transcription regulator [Lactobacillus plantarum WCFS1]
emb|CAD65154.1| transcription regulator [Lactobacillus plantarum WCFS1]
Length=178

GENE ID: 1063436 lp_2967 | transcription regulator [Lactobacillus plantarum WCFS1] (10 or fewer PubMed links)

Score = 50.1 bits (118), Expect = 6e-05, Method: Compositional matrix adjust.
Identities = 33/104 (31%), Positives = 57/104 (54%), Gaps = 5/104 (4%)

```
Query  39   QEHILMLLAEQIS--TNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSL  96
            Q  IL +LA+   +  TNA+IAE L I P++V+  L +L++  LI+   + +D+RVV+  L
Sbjct  43   QMGILRVLADAPAGLTNAEIAEILDIRPSSVSATLNRLEDGGLIEREPSAHDKRVVIVRL  102
```

```
Query  97   TEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSAL  140
            +++   +A   A   + T     +L    TD+E+  +   L  L
Sbjct  103  SDRGREMADHRA---QGTSDLADQLFGNLTDDERNQLQHLLDKL  143
```

>**ref|YP_757477.1|** MarR family transcriptional regulator [Maricaulis maris MCS10]
gb|ABI66539.1| transcriptional regulator, MarR family [Maricaulis maris MCS10]
Length=143

GENE ID: 4285355 Mmar10_2247 | MarR family transcriptional regulator [Maricaulis maris MCS10]

Score = 50.1 bits (118), Expect = 6e-05, Method: Compositional matrix adjust.
Identities = 39/146 (26%), Positives = 75/146 (51%), Gaps = 5/146 (3%)

```
Query  1    MSLANQIDQFLGTIMQFAENK-HEILLGKCESDVKLTSTQEHILMLLAEQISTN-AKIAE  58
            M+ A  +D+ L  +++ A  K +     + +S   +TS Q  +L LLA +        I E
Sbjct  1    MARARAVDRRLFLLLEIAARKLNRDADARLKSVAGVTSAQAAVLFLLARRGERRMGDIGE  60

Query  59   KLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTY  118
             L + P AVT  + +++   L+    + +D+R  + SLTEK   +  + A H  + L+T
Sbjct  61   MLSLHPPAVTGLVNRMEALGLVTKKTSPSDKRSAIVSLTEKGRALG-DTADHILRDLNT-  118

Query  119  QELGNKFTDEEQEVISKFLSALTEEF  144
              EL N+  +E+ +++ + L+ +  +F
Sbjct  119  -ELENRLGEEDADMLHRVLTRIAVDF  143
```

>**ref|NP_391385.1|** hypothetical protein BSU35050 [Bacillus subtilis subsp. subtilis str. 168]
ref|ZP_03593302.1| hypothetical protein Bsubs1_18971 [Bacillus subtilis subsp. subtilis str. 168]
ref|ZP_03597587.1| hypothetical protein BsubsN3_18887 [Bacillus subtilis subsp. subtilis str. NCIB 3610]
ref|ZP_03601991.1| hypothetical protein BsubsJ_18850 [Bacillus subtilis subsp. subtilis str. JH642]
ref|ZP_03606276.1| hypothetical protein BsubsS_19006 [Bacillus subtilis subsp. subtilis str. SMY]
sp|O34692.1|YVNA_BACSU RecName: Full=Uncharacterized HTH-type transcriptional regulator yvnA
gb|AAC67281.1| YvnA [Bacillus subtilis]
emb|CAB15510.1| yvnA [Bacillus subtilis subsp. subtilis str. 168]
Length=157

GENE ID: 936639 yvnA | yvnA [Bacillus subtilis subsp. subtilis str. 168] (10 or fewer PubMed links)

Score = 50.1 bits (118), Expect = 6e-05, Method: Compositional matrix adjust.
Identities = 30/104 (28%), Positives = 59/104 (56%), Gaps = 1/104 (0%)

```
Query  36   TSTQEHILMLL-AEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLW  94
            T TQ HI+  +   Q   N+ +A +L IS AAV+KA+  L +  +I  ++   +++ + +
Sbjct  48   TLTQLHIVSCIHTSQNVNNSFLASRLHISKAAVSKAVHALLKHNIITVTKKPGNKKEIFY  107

Query  95   SLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLS  138
            +LT+    +A  H   HEK    Y++L N+F+ ++ + ++ ++ F +
Sbjct  108  TLTDSGRKLAALHEQLHEKAKEQYKQLFNEFSIDDLKTVTAFFN  151
```

>**ref|NP_111681.1|** transcription regulator (SlyA-related) [Thermoplasma volcanium GSS1]
dbj|BAB60329.1| hypothetical protein [Thermoplasma volcanium GSS1]
Length=143

GENE ID: 1441302 TVN1162 | transcription regulator (SlyA-related) [Thermoplasma volcanium GSS1] (10 or fewer PubMed links)

Score = 49.7 bits (117), Expect = 7e-05, Method: Compositional matrix adjust.
Identities = 30/81 (37%), Positives = 45/81 (55%), Gaps = 0/81 (0%)

```
Query  26   LGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRA  85
            +G+  S +     +  IL LL+E  ST  K+AE   ++PA +T  L +++ Q LI  SR+
Sbjct  27   MGESLSHISAKPIEVRILYLLSEDESTVNKLAELTDVTPAWITGTLDEMESQGLIVRSRS  86

Query  86   TNDERVVLWSLTEKAVPVAKE  106
              D RVV   +TEK + V  E
Sbjct  87   GEDRRVVNVHITEKGIEVLNE  107
```

>**ref|NP_419215.1|** MarR family transcriptional regulator [Caulobacter crescentus CB15]
ref|YP_002515775.1| transcriptional regulator, MarR family [Caulobacter crescentus NA1000]
gb|AAK22383.1| transcriptional regulator, MarR family [Caulobacter crescentus CB15]
gb|ACL93867.1| transcriptional regulator, MarR family [Caulobacter crescentus NA1000]
Length=147

GENE ID: 942105 CC_0396 | MarR family transcriptional regulator [Caulobacter crescentus CB15] (10 or fewer PubMed links)

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```
 Score = 49.3 bits (116),  Expect = 9e-05, Method: Compositional matrix adjust.
 Identities = 32/119 (26%), Positives = 63/119 (52%), Gaps = 4/119 (3%)

Query  27   GKCESDVKLTSTQEHILMLLAEQIST-NAKIAEKLKISPAAVTKALKKLQEQELIKSSRA  85
            G+  ++  LT+ Q  +L  L E+      + A+ L ++P+A+T  + ++   EL++
Sbjct  26   GRMAAEGGLTAAQSGVLFFLGERDGALIGEAADALDLAPSAMTGLIDRMARAELVERRAD  85

Query  86   TNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF  144
              D R +   LT+K    A++ A    + ++   +L   FTDEE  V+S++L++L  +F
Sbjct  86   AKDGRAMHLHLTDKGR-AARDTAKAGLRGVNA--QLTEGFTDEEISVVSRWLASLQTKF  141


>ref|YP_001031482.1| G MarR family transcriptional regulator [Lactococcus lactis subsp.
cremoris MG1363]
 emb|CAL96727.1| G transcriptional regulator, MarR family [Lactococcus lactis subsp.
cremoris MG1363]
Length=172

 GENE ID: 4798609 rmaD | MarR family transcriptional regulator
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

 Score = 49.3 bits (116),  Expect = 1e-04, Method: Compositional matrix adjust.
 Identities = 26/98 (26%), Positives = 55/98 (56%), Gaps = 0/98 (0%)

Query  41   HILMLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKA  100
            HIL  L ++  T  ++A KL ++   VT+A++ L + + + + +A ND++ + + +T K
Sbjct  56   HILSALTKKDLTGIELATKLSVTRGGVTRAVQNLIKHQFLTTYQADNDKKKIYYHITTKG  115

Query  101  VPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLS  138
            + VA  H   H+        ++ +K+ + ++ +I  FLS
Sbjct  116  LKVASIHDKMHKIMDLKLGQIFDKYNENDKSIILNFLS  153


>ref|NP_603578.1| G MarR family transcriptional regulator [Fusobacterium nucleatum
subsp. nucleatum ATCC 25586]
 gb|AAL94877.1| G Transcriptional regulator, MarR family [Fusobacterium nucleatum
subsp. nucleatum ATCC 25586]
Length=225

 GENE ID: 991648 FN0681 | MarR family transcriptional regulator
[Fusobacterium nucleatum subsp. nucleatum ATCC 25586] (10 or fewer PubMed links)

 Score = 48.9 bits (115),  Expect = 1e-04, Method: Compositional matrix adjust.
 Identities = 29/88 (32%), Positives = 50/88 (56%), Gaps = 3/88 (3%)

Query  35   LTSTQEHILMLLAE--QISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVV  92
            LT T+ HI+   + E  Q++ N ++A+K+ I+    T A+ KL ++  I  +R+T D R V
Sbjct  34   LTHTELHIIESIGENTQLTMN-ELADKIGITMGTATVAISKLSDKGYIDRARSTTDRRKV  92

Query  93   LWSLTEKAVPVAKEHATHHEKTLSTYQE  120
              SLT+K V      H  +H+  +++  E
Sbjct  93   FVSLTKKGVDALTYHNNYHKMIMASITE  120


>ref|YP_138915.1| G MarR family transcriptional regulator [Streptococcus thermophilus
LMG 18311]
 gb|AAV60100.1| G transcriptional regulator, MarR family [Streptococcus thermophilus
LMG 18311]
Length=144

 GENE ID: 3164787 stu0381 | MarR family transcriptional regulator
[Streptococcus thermophilus LMG 18311] (10 or fewer PubMed links)

 Score = 48.9 bits (115),  Expect = 1e-04, Method: Compositional matrix adjust.
 Identities = 31/90 (34%), Positives = 51/90 (56%), Gaps = 3/90 (3%)

Query  51   STNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATH  110
            +T + +A +L ++   VT +L KL+++  I  +R++ D RVV  SL++K   V + H
Sbjct  50   TTPSAVARELMLTLGTVTTSLNKLEKKGYIIRTRSSVDRRVVHLSLSKKGRLVYRLHRGF  109

Query  111  HEKTLSTYQELGNKFTDEEQEVISKFLSAL  140
            H+  + T  E    F DEE +V+SK L  L
Sbjct  110  HKSMVKTITE---GFNDEELKVMSKGLENL  136


>ref|YP_002165566.1| G possible MarR family transcriptional regulator [Fusobacterium
nucleatum subsp. polymorphum ATCC 10953]
 gb|EDK89119.1| G possible MarR family transcriptional regulator [Fusobacterium
nucleatum subsp. polymorphum ATCC 10953]
Length=225

 GENE ID: 6818656 FNP_1336 | possible MarR family transcriptional regulator
[Fusobacterium nucleatum subsp. polymorphum ATCC 10953]

 Score = 48.9 bits (115),  Expect = 1e-04, Method: Compositional matrix adjust.
 Identities = 29/88 (32%), Positives = 50/88 (56%), Gaps = 3/88 (3%)

Query  35   LTSTQEHILMLLAE--QISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVV  92
            LT T+ HI+   + E  Q++ N ++A+K+ I+    T A+ KL ++  I  +R+T D R V
Sbjct  34   LTHTELHIIESIGENTQLTMN-ELADKIGITMGTATVAISKLSDKGYIDRARSTTDRRKV  92

Query  93   LWSLTEKAVPVAKEHATHHEKTLSTYQE  120
              SLT+K V      H  +H+  +++  E
```

```
Sbjct  93   FVSLTKKGVDALTYHNNYHKMIMASITE  120
```

>ref|ZP_00144611.1| Transcriptional regulator, MarR family [Fusobacterium nucleatum subsp. vincentii ATCC 49256]
gb|EAA23791.1| Transcriptional regulator, MarR family [Fusobacterium nucleatum subsp. vincentii ATCC 49256]
Length=225

Score = 48.9 bits (115), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 29/88 (32%), Positives = 50/88 (56%), Gaps = 3/88 (3%)

```
Query  35   LTSTQEHILMLLAE--QISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVV  92
            LT T+ HI+  + E  Q++ N ++A+K+ I+    T A+ KL ++  I  +R+T D R V
Sbjct  34   LTHTELHIIESIGENTQLTMN-ELADKIGITMGTATVAISKLSDKGYIDRARSTTDRRKV  92

Query  93   LWSLTEKAVPVAKEHATHHEKTLSTYQE  120
              SLT+K V     H  +H+  +++  E
Sbjct  93   FVSLTKKGVDALTYHNNYHKMIMASITE  120
```

>ref|YP_819912.1| MarR family transcriptional regulator [Streptococcus thermophilus LMD-9]
gb|ABJ65716.1| transcriptional regulator, MarR family [Streptococcus thermophilus LMD-9]
Length=144

GENE ID: 4437359 STER_0428 | MarR family transcriptional regulator [Streptococcus thermophilus LMD-9] (10 or fewer PubMed links)

Score = 48.9 bits (115), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 31/90 (34%), Positives = 51/90 (56%), Gaps = 3/90 (3%)

```
Query  51   STNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATH  110
            +T + +A +L ++   VT +L KL+++  I  +R++ D RVV  SL++K   V + H
Sbjct  50   TTPSAVARELMLTLGTVTTSLNKLEKKGYIIRTRSSVDRRVVHLSLSKKGRLVYRLHRAF  109

Query  111  HEKTLSTYQELGNKFTDEEQEVISKFLSAL  140
            H+  + T  E    F DEE +V+SK L  L
Sbjct  110  HKSMVKTITE---GFNDEELKVMSKGLENL  136
```

>ref|YP_079349.1| transcriptional regulator YvmB [Bacillus licheniformis ATCC 14580]
gb|AAU23711.1| possible transcriptional regulator YvmB [Bacillus licheniformis ATCC 14580]
Length=161

GENE ID: 3031484 yvmB | transcriptional regulator YvmB [Bacillus licheniformis ATCC 14580] (10 or fewer PubMed links)

Score = 48.5 bits (114), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 35/117 (29%), Positives = 59/117 (50%), Gaps = 4/117 (3%)

```
Query  29   CESDVKL---TSTQEHILMLLA-EQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSR  84
             ESDVK      T  H++  +  ++   N  IA+K+ +S A +TK   KL ++ LIK  +
Sbjct  36   AESDVKRLPGNMTTIHVISCIGHDEPINNTGIAKKMNLSKANITKISSKLLKEGLIKRFQ  95

Query  85   ATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALT  141
             T++++ + + LT     V + H   H++    +  + F+  EQ  I KFL  LT
Sbjct  96   LTDNKKEIYFRLTPSGKQVFELHEKLHQQKADQFSRFLDSFSTAEQGAILKFLQGLT  152
```

>ref|ZP_01219563.1| putative transcriptional regulator, MarR family protein [Photobacterium profundum 3TCK]
gb|EAS43796.1| putative transcriptional regulator, MarR family protein [Photobacterium profundum 3TCK]
Length=138

Score = 48.1 bits (113), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 39/143 (27%), Positives = 73/143 (51%), Gaps = 13/143 (9%)

```
Query  7    IDQFLGTIMQFAEN----KHEILLGKCESDVKLTSTQEHILMLLAEQISTNAK-IAEKLK  61
            I+Q   TI++F E     +  ++ GK       +  Q HI+ +L    +   K +A+K+
Sbjct  4    IEQLNHTIIEFYEKLSSWEQSVVRGKG-----FSLPQVHIVEILGAHGAMRMKELADKIG  58

Query  62   ISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQEL  121
            ++   +T  + K+ + ELI+     +D R +L  LTEK V + +EH   H   LS  Q++
Sbjct  59   VTTGTLTVQVDKMVQAELIQRRPHESDRRSILVDLTEKGVEMYQEHDHLH---LSLTQDI  115

Query  122  GNKFTDEEQEVISKFLSALTEEF  144
              +  D E++ +  +L+ + +EF
Sbjct  116  TAQLDDVERKNLLMYLTKMNQEF  138
```

>ref|YP_091766.1| YvmB [Bacillus licheniformis ATCC 14580]
gb|AAU41073.1| YvmB [Bacillus licheniformis DSM 13]
Length=163

GENE ID: 3097946 yvmB | YvmB [Bacillus licheniformis ATCC 14580] (10 or fewer PubMed links)

Score = 48.1 bits (113), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 35/117 (29%), Positives = 59/117 (50%), Gaps = 4/117 (3%)

```
Query  29   CESDVKL---TSTQEHILMLLA-EQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSR  84
            ESDVK      T  H++  +  ++   N  IA+K+ +S A +TK   KL ++ LIK  +
Sbjct  38   AESDVKRLPGNMTTIHVISCIGHDEPINNTGIAKKMNLSKANITKISSKLLKEGLIKRFQ  97

Query  85   ATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALT  141
            T++++ + + LT     V + H   H++    +    + F+  EQ  I KFL  LT
Sbjct  98   LTDNKKEIYFRLTPSGKQVFELHEKLHQQKADQFSRFLDSFSTAEQGAILKFLQGLT  154


>ref|YP_129221.1| G MarR family transcriptional regulator [Photobacterium profundum
SS9]
 emb|CAG19419.1| G putative transcriptional regulator, MarR family [Photobacterium
profundum SS9]
Length=138

 GENE ID: 3122954 PBPRA1008 | MarR family transcriptional regulator
[Photobacterium profundum SS9] (10 or fewer PubMed links)

 Score = 48.1 bits (113),  Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 39/143 (27%), Positives = 73/143 (51%), Gaps = 13/143 (9%)

Query  7    IDQFLGTIMQFAEN----KHEILLGKCESDVKLTSTQEHILMLLAEQISTNAK-IAEKLK  61
            I+Q   TI++F E     +  ++ GK       +  Q HI+ +L    +   K +A+K+
Sbjct  4    IEQLNHTIIEFYEKLSSWEQSVVRGKG-----FSLPQIHIVEILGAHGAMRMKELADKIG  58

Query  62   ISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQEL  121
            ++   +T  + K+ + ELI+     +D R +L  LTE+ V + +EH   H   LS  Q++
Sbjct  59   VTTGTLTVQVDKMVQAELIQRRPHESDRRSILVDLTEQGVEMYQEHDHLH---LSLTQDI  115

Query  122  GNKFTDEEQEVISKFLSALTEEF  144
              K  D E++ +  +L+ + +EF
Sbjct  116  TAKLDDTERKNLLMYLTKMNQEF  138


>ref|ZP_00990845.1|  hypothetical transcriptional regulator, MarR family [Vibrio splendidus
12B01]
 gb|EAP94213.1|  hypothetical transcriptional regulator, MarR family [Vibrio splendidus
12B01]
Length=301

 Score = 48.1 bits (113),  Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 35/117 (29%), Positives = 62/117 (52%), Gaps = 1/117 (0%)

Query  25   LLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSR  84
            +L K   D+ L   Q H L+ L +Q  T  ++A+KL I  +  ++A+  L +  LI++S
Sbjct  19   MLDKDCGDIALPPIQAHTLIELEQQPLTVNQLADKLNIDKSNASRAVNNLAKNSLIQTSP  78

Query  85   ATNDERVVLWSLTEKAV-PVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSAL  140
              ND+R V+ S+TE+ +  +A+ H+  ++   S  + L    T +    I  +L AL
Sbjct  79   HPNDKRSVVASVTEQGIKTLAQLHSQQNQFYDSVLERLTEAETQQVSGGIKHYLKAL  135


>ref|YP_001319891.1| G MarR family transcriptional regulator [Alkaliphilus metalliredigens
QYMF]
 gb|ABR48232.1| G transcriptional regulator, MarR family [Alkaliphilus metalliredigens
QYMF]
Length=143

 GENE ID: 5312143 Amet_2072 | MarR family transcriptional regulator
[Alkaliphilus metalliredigens QYMF]

 Score = 47.8 bits (112),  Expect = 3e-04, Method: Compositional matrix adjust.
 Identities = 27/67 (40%), Positives = 42/67 (62%), Gaps = 1/67 (1%)

Query  35   LTSTQEHILMLLAEQISTNAK-IAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVL  93
            +T TQ   L++L E+    AK + EKL +    +T  LKKL+ +ELI   R+T DER+++
Sbjct  37   ITYTQYITLLVLWEKPKITAKELGEKLYLDSGTLTPLLKKLESKELITRKRSTKDERIMI  96

Query  94   WSLTEKA  100
             +LT+K
Sbjct  97   VTLTDKG  103


>ref|YP_001838202.1| G MarR family transcriptional regulator [Leptospira biflexa serovar
Patoc strain 'Patoc 1 (Paris)']
 gb|ABZ96926.1| G Putative transcriptional regulator, MarR family [Leptospira biflexa
serovar Patoc strain 'Patoc 1 (Paris)']
Length=133

 GENE ID: 6222463 LEPBI_I0798 | MarR family transcriptional regulator
[Leptospira biflexa serovar Patoc strain 'Patoc 1 (Paris)']
(10 or fewer PubMed links)

 Score = 47.8 bits (112),  Expect = 3e-04, Method: Compositional matrix adjust.
 Identities = 26/71 (36%), Positives = 45/71 (63%), Gaps = 1/71 (1%)

Query  31   SDVKLTSTQEHILMLLAEQ-ISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDE  89
            +D+ LT  Q  +++++ E+ IST +KI +KL++    +T  LK+L++ EL+   R  NDE
Sbjct  26   ADLGLTYPQYLVMLVMWEEKISTVSKIGDKLQLDSGTLTPLLKRLEQMELLDRMRNPNDE  85

Query  90   RVVLWSLTEKA  100
            R V   L++K
Sbjct  86   RSVNIVLSKKG  96
```

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>ref|YP_108512.1| putative transcriptional regulatory protein [Burkholderia pseudomallei K96243]
ref|YP_102754.1| MarR family transcriptional regulator [Burkholderia mallei ATCC 23344]
ref|ZP_00438156.1| COG1846: Transcriptional regulators [Burkholderia mallei GB8 horse 4]
46 more sequence titles

ref|YP_333321.1| MarR family transcriptional regulator [Burkholderia pseudomallei 1710b]
ref|YP_992831.1| MarR family transcriptional regulator [Burkholderia mallei SAVP1]
ref|YP_001026174.1| MarR family transcriptional regulator [Burkholderia mallei NCTC 10229]
ref|YP_001058785.1| MarR family transcriptional regulator [Burkholderia pseudomallei 668]
ref|YP_001080556.1| MarR family transcriptional regulator [Burkholderia mallei NCTC 10247]
ref|YP_001066038.1| MarR family transcriptional regulator [Burkholderia pseudomallei 1106a]
ref|ZP_01769009.1| transcriptional regulator, MarR family [Burkholderia pseudomallei 305]
ref|ZP_02102319.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei 1106b]
ref|ZP_02109049.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei 1710a]
ref|ZP_02266811.1| transcriptional regulator, MarR family protein [Burkholderia mallei PRL-20]
ref|ZP_02403045.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei DM98]
ref|ZP_02411585.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei 14]
ref|ZP_02447714.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei 91]
ref|ZP_02455880.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei 9]
ref|ZP_02471448.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei B7210]
ref|ZP_02481920.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei 7894]
ref|ZP_02490126.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei NCTC 13177]
ref|ZP_02498250.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei 112]
ref|ZP_02506273.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei BCC215]
ref|YP_002009903.1| transcriptional regulator, MarR family [Burkholderia mallei ATCC 10399]
ref|YP_002036065.1| transcriptional regulator, MarR family [Burkholderia pseudomallei 1655]
ref|YP_002022669.1| transcriptional regulator, MarR family [Burkholderia pseudomallei Pasteur 52237]
ref|YP_002050288.1| transcriptional regulator, MarR family [Burkholderia pseudomallei S13]
ref|YP_002060819.1| transcriptional regulator, MarR family [Burkholderia mallei FMH]
ref|YP_002064980.1| transcriptional regulator, MarR family [Burkholderia mallei JHU]
ref|YP_002106328.1| transcriptional regulator, MarR family [Burkholderia pseudomallei 406e]
ref|YP_002110157.1| transcriptional regulator, MarR family [Burkholderia mallei 2002721280]
ref|ZP_03454874.1| transcriptional regulator, MarR family [Burkholderia pseudomallei 576]
emb|CAH35912.1| putative transcriptional regulatory protein [Burkholderia pseudomallei K96243]
gb|AAU48847.1| transcriptional regulator, MarR family [Burkholderia mallei ATCC 23344]
gb|ABA50381.1| transcriptional regulator, MarR family [Burkholderia pseudomallei 1710b]
gb|ABM52457.1| transcriptional regulator, MarR family [Burkholderia mallei SAVP1]
gb|ABN02741.1| transcriptional regulator, MarR family [Burkholderia mallei NCTC 10229]
gb|ABN82036.1| transcriptional regulator, MarR family [Burkholderia pseudomallei 668]
gb|ABN89050.1| transcriptional regulator, MarR family [Burkholderia pseudomallei 1106a]
gb|ABO05799.1| transcriptional regulator, MarR family [Burkholderia mallei NCTC 10247]
gb|EBA46431.1| transcriptional regulator, MarR family [Burkholderia pseudomallei 305]
gb|EDK56373.1| transcriptional regulator, MarR family [Burkholderia mallei FMH]
gb|EDK60534.1| transcriptional regulator, MarR family [Burkholderia mallei JHU]
gb|EDK85546.1| transcriptional regulator, MarR family [Burkholderia mallei 2002721280]
gb|EDO84870.1| transcriptional regulator, MarR family [Burkholderia pseudomallei

406e]
gb|EDO91962.1| transcriptional regulator, MarR family [Burkholderia pseudomallei Pasteur 52237]
gb|EDP89187.1| transcriptional regulator, MarR family [Burkholderia mallei ATCC 10399]
gb|EDS86631.1| transcriptional regulator, MarR family [Burkholderia pseudomallei S13]
gb|EDU07559.1| transcriptional regulator, MarR family [Burkholderia pseudomallei 1655]
gb|EEC33252.1| transcriptional regulator, MarR family [Burkholderia pseudomallei 576]
Length=165

GENE ID: 3092472 BPSL1912 | putative transcriptional regulatory protein [Burkholderia pseudomallei K96243] (10 or fewer PubMed links)

Score = 47.4 bits (111), Expect = 4e-04, Method: Compositional matrix adjust.
Identities = 33/126 (26%), Positives = 69/126 (54%), Gaps = 5/126 (3%)

```
Query  6    QIDQFLGTIMQFAEN-KHEILLGKCESDVKLTSTQEHILMLLA-EQISTNAKIAEKLKIS  63
            QI+  +G +M   ++    ++  + ++++ +T TQ  +L +LA  + ST A++A +  I
Sbjct  17   QINDSVGYLMSRVKSLMTNMVTQRTQTELGITGTQATMLFMLAVGKCSTAAELAREYGID  76

Query  64   PAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGN  123
             +A+T+ L +++++ L++  R++ D RVV   LT++   + K          L    E+ +
Sbjct  77   ASAITRLLDRVEKRGLLQRVRSSEDRRVVRLELTDEGRALTKRMPAIFRSVL---DEVLD  133

Query  124  KFTDEE  129
             FT EE
Sbjct  134  GFTPEE  139
```

>ref|YP_001961880.1| Transcriptional regulator, marR family [Leptospira biflexa serovar Patoc strain 'Patoc 1 (Ames)']
gb|ABZ93302.1| Transcriptional regulator, marR family [Leptospira biflexa serovar Patoc strain 'Patoc 1 (Ames)']
Length=145

GENE ID: 6388419 LBF_0770 | Transcriptional regulator, marR family [Leptospira biflexa serovar Patoc strain 'Patoc 1 (Ames)'] (10 or fewer PubMed links)

Score = 47.4 bits (111), Expect = 4e-04, Method: Compositional matrix adjust.
Identities = 26/71 (36%), Positives = 45/71 (63%), Gaps = 1/71 (1%)

```
Query  31   SDVKLTSTQEHILMLL-AEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDE  89
            +D+ LT  Q  +++++  E+IST +KI +KL++     +T  LK+L++ EL+   R  NDE
Sbjct  38   ADLGLTYPQYLVMLVMWEEKISTVSKIGDKLQLDSGTLTPLLKRLEQMELLDRMRNPNDE  97

Query  90   RVVLWSLTEKA  100
            R V   L++K
Sbjct  98   RSVNIVLSKKG  108
```

>ref|YP_001310724.1| MarR family transcriptional regulator [Clostridium beijerinckii NCIMB 8052]
gb|ABR35768.1| transcriptional regulator, MarR family [Clostridium beijerinckii NCIMB 8052]
Length=155

GENE ID: 5294814 Cbei_3649 | MarR family transcriptional regulator [Clostridium beijerinckii NCIMB 8052]

Score = 47.4 bits (111), Expect = 4e-04, Method: Compositional matrix adjust.
Identities = 30/109 (27%), Positives = 57/109 (52%), Gaps = 1/109 (0%)

```
Query  34   KLTSTQEHILMLLAEQISTN-AKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVV  92
            KLT +Q H +  +       N  K++++L ++  A+TK  KKL  +  +   + + + V
Sbjct  28   KLTFSQIHCIAAIEYIEDANITKLSQELGMTTGAITKMCKKLLNEGYVSKYQKEGNNKEV  87

Query  93   LWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALT  141
             + LTE  + V + H    HEK+ +  +++  ++ DEE+  I KFL  +
Sbjct  88   YYDLTELGLNVCEIHNRIHEKSYNKKKDIIAQYNDEEKATILKFLHDMN  136
```

>ref|ZP_01065868.1| hypothetical transcriptional regulator, MarR family protein [Vibrio sp. MED222]
gb|EAQ52745.1| hypothetical transcriptional regulator, MarR family protein [Vibrio sp. MED222]
Length=301

Score = 47.0 bits (110), Expect = 5e-04, Method: Compositional matrix adjust.
Identities = 26/77 (33%), Positives = 45/77 (58%), Gaps = 0/77 (0%)

```
Query  25   LLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSR  84
            +L K   D+ L   Q H L+ L +Q  T  ++A+KL I  +  ++A+  L +  LI++S
Sbjct  19   MLDKDCGDIALPPIQAHTLIELEQQPLTVNQLADKLNIDKSNASRAVNNLAKNSLIQTSP  78

Query  85   ATNDERVVLWSLTEKAV  101
              ND+R V+ S+TE+ +
Sbjct  79   HPNDKRSVVASVTEQGI  95
```

Annex 1

>**ref|YP_140799.1|** MarR family transcriptional regulator [Streptococcus thermophilus CNRZ1066]
gb|AAV61984.1| transcriptional regulator, MarR family [Streptococcus thermophilus CNRZ1066]
Length=144

GENE ID: 3167129 str0381 | MarR family transcriptional regulator [Streptococcus thermophilus CNRZ1066] (10 or fewer PubMed links)

Score = 47.0 bits (110), Expect = 5e-04, Method: Compositional matrix adjust.
Identities = 30/90 (33%), Positives = 50/90 (55%), Gaps = 3/90 (3%)

```
Query  51   STNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATH  110
            +T + +A +L ++    VT +L KL+++  I  +R++ D RVV  SL++K   V + H
Sbjct  50   TTPSAVARELMLTLGTVTTSLNKLEKKGYIIRTRSSVDRRVVHLSLSKKGRLVYRLHRGF  109

Query  111  HEKTLSTYQELGNKFTDEEQEVISKFLSAL  140
            H+   S    +   F DEE +V+SK L  L
Sbjct  110  HK---SMVMRITEGFNDEELKVMSKGLENL  136
```

>**ref|YP_143999.1|** MarR family transcriptional regulator [Thermus thermophilus HB8]
dbj|BAD70556.1| transcriptional regulator MarR family [Thermus thermophilus HB8]
Length=144

GENE ID: 3168756 TTHA0733 | MarR family transcriptional regulator [Thermus thermophilus HB8]

Score = 46.6 bits (109), Expect = 6e-04, Method: Compositional matrix adjust.
Identities = 34/109 (31%), Positives = 55/109 (50%), Gaps = 5/109 (4%)

```
Query  35   LTSTQEHILMLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLW  94
            L+  + H+L LLA+ +   +++AE L++ P+ V+  L  L+E+ L+K S    D R V
Sbjct  36   LSPRKAHLLGLLAKGVDLPSQLAELLEVHPSQVSHLLAALEEEGLVKRSPDPQDRRKVKL  95

Query  95   SLTEKAVPVAKEHATHHEKT-LSTYQELGNKFTDEEQEVISKFLSALTE  142
             LT    P  +E A   E   L+ +     + + EEQ    + L  LTE
Sbjct  96   FLT----PKGREAAARTEALWLAVFGRRLARLSPEEQAAFLRILRKLTE  140
```

>**ref|YP_293371.1|** regulatory protein, MarR [Ralstonia eutropha JMP134]
gb|AAZ65514.1| regulatory protein, MarR [Ralstonia eutropha JMP134]
Length=150

GENE ID: 3607869 Reut_C6203 | regulatory protein, MarR [Ralstonia eutropha JMP134]

Score = 46.6 bits (109), Expect = 7e-04, Method: Compositional matrix adjust.
Identities = 32/112 (28%), Positives = 58/112 (51%), Gaps = 1/112 (0%)

```
Query  6    QIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNA-KIAEKLKISP  64
            +I Q +G  +  A N   + +     D+ +T  Q  IL+ L + ++T   ++++ L I
Sbjct  15   RITQSVGFFLNRARNTLLMEMDAALKDLDITGQQMGILLSLTQGVATTPFELSKVLGIDT  74

Query  65   AAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLS  116
              +T+ L KL+ + L+  SR+ +D RVV  +LT+K   VA+       K L+
Sbjct  75   GLMTRMLDKLETKGLLSRSRSLDDRRVVNLTLTQKGQEVAERAPVVAPKVLN  126
```

>**ref|YP_001307422.1|** MarR family transcriptional regulator [Clostridium beijerinckii NCIMB 8052]
gb|ABR32466.1| transcriptional regulator, MarR family [Clostridium beijerinckii NCIMB 8052]
Length=153

GENE ID: 5291510 Cbei_0278 | MarR family transcriptional regulator [Clostridium beijerinckii NCIMB 8052]

Score = 46.6 bits (109), Expect = 7e-04, Method: Compositional matrix adjust.
Identities = 30/114 (26%), Positives = 62/114 (54%), Gaps = 1/114 (0%)

```
Query  32   DVKLTSTQEHILMLLAEQISTNAK-IAEKLKISPAAVTKALKKLQEQELIKSSRATNDER  90
            D+ L  ++ H++  + +    NA  I+++L ++  A++K   KL ++ELIK +   N+++
Sbjct  40   DMGLMLSEIHVIDCIGKNQLINATFISKELNMTKGAISKITSKLLKKELIKGNHLENNKK  99

Query  91   VVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF  144
             + ++LT +   V K H   H+    + ++ +K+  EE  +I+ FL  L  E
Sbjct  100  EIYYTLTAQGKEVFKVHEILHKIESEKFVKILSKYDKEELSIINSFLEDLISEL  153
```

>**ref|ZP_02950515.1|** transcriptional regulator, MarR family [Clostridium butyricum 5521]
gb|EDT74473.1| transcriptional regulator, MarR family [Clostridium butyricum 5521]
Length=145

Score = 46.2 bits (108), Expect = 8e-04, Method: Compositional matrix adjust.
Identities = 32/86 (37%), Positives = 48/86 (55%), Gaps = 2/86 (2%)

```
Query  17   FAENKHEILLGK-CESDVKLTSTQE-HILMLLAEQISTNAKIAEKLKISPAAVTKALKKL  74
            +A ++  I L K C     LT TQ   +L+L  ++ ST  +I ++L +    +T  LKK+
Sbjct  19   YAASREVIKLYKPCLDKFNLTYTQYVAMLVLWEDEKSTVKEIGKRLHLDSGTLTPLLKKM  78
```

```
Query  75   QEQELIKSSRATNDERVVLWSLTEKA  100
            +  ELIK   R  ND+RVV+  L EK
Sbjct  79   ESMELIKRYRDINDDRVVIVELAEKG  104
```

>**ref|NP_266269.1|** transcription regulator [Lactococcus lactis subsp. lactis Il1403]
gb|AAK04211.1|AE006249_8 transcriptional regulator [Lactococcus lactis subsp. lactis Il1403]
Length=163

GENE ID: 1113719 rmaD | transcription regulator
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 46.2 bits (108), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 26/98 (26%), Positives = 55/98 (56%), Gaps = 0/98 (0%)

```
Query  41   HILMLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKA  100
            HIL  L ++  T  ++A KL ++   VT+A++ L + + + + ++ +D++ + + LT K
Sbjct  53   HILSALTKEDLTGIELATKLSVTRGGVTRAVQNLIKYQFLTTYQSESDKKKIFYHLTVKG  112

Query  101  VPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLS  138
             VA  H   H+       ++ +K+ ++E+ +I  FLS
Sbjct  113  RKVATIHDKMHKIMDIRLGQIFDKYNEQEKSIILSFLS  150
```

>**ref|YP_002352539.1|** transcriptional regulator, MarR family [Dictyoglomus turgidum DSM 6724]
gb|ACK41925.1| transcriptional regulator, MarR family [Dictyoglomus turgidum DSM 6724]
Length=145

GENE ID: 7081680 Dtur_0640 | transcriptional regulator, MarR family
[Dictyoglomus turgidum DSM 6724]

Score = 46.2 bits (108), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 33/118 (27%), Positives = 63/118 (53%), Gaps = 8/118 (6%)

```
Query  31   SDVKLTSTQEHILMLLAEQIS-TNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDE  89
            S +KL   Q  IL+LL+E+   T  +I E +KI P+ V   +++++++ L+ + R   D+
Sbjct  26   SGLKLYRGQAPILLLLSERDGLTQKEIVENMKIKPSTVAIMIRRMKKRGLVITKRDEKDK  85

Query  90   RVVLWSLTEKAVPVAKEHATHHEKTLSTYQE--LGNKFTDEEQEVISKFLSALTEEFQ  145
            R     LT++     ++     +KT    +E   GN FT+EE+E +  +L  + +  +
Sbjct  86   RFSKVYLTDE----GRKFICKLKKTYKQLEEECFGN-FTEEERETLKNYLERIRDNLR  138
```

>**ref|ZP_01854255.1|** probable marR-family transcription regulator [Planctomyces maris DSM 8797]
gb|EDL59963.1| probable marR-family transcription regulator [Planctomyces maris DSM 8797]
Length=159

Score = 46.2 bits (108), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 29/83 (34%), Positives = 46/83 (55%), Gaps = 2/83 (2%)

```
Query  26   LGKCESDVKLTSTQEHILMLLA--EQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSS  83
             G+   +  LT +Q ++L +L    +   + +IA ++     A+T  L +LQ QELIK +
Sbjct  38   FGRLFREYGLTPSQYNVLRILRGERKPMPSLEIANRMIQVVPAITGLLDRLQAQELIKRN  97

Query  84   RATNDERVVLWSLTEKAVPVAKE  106
            R T D RVV   +T KA+ + KE
Sbjct  98   RCTEDRRVVYIEITAKALKLLKE  120
```

>**ref|YP_773280.1|** MarR family transcriptional regulator [Burkholderia ambifaria AMMD]
gb|ABI86946.1| transcriptional regulator, MarR family [Burkholderia ambifaria AMMD]
Length=164

GENE ID: 4309612 Bamb_1388 | MarR family transcriptional regulator
[Burkholderia ambifaria AMMD]

Score = 45.8 bits (107), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 31/118 (26%), Positives = 59/118 (50%), Gaps = 4/118 (3%)

```
Query  28   KCESDVKLTSTQEHILMLLA-EQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRAT  86
            + + ++ +T TQ  +L ++A  + ST A++A +  I  +AVT+ L +++++  L+   R+
Sbjct  40   RTQEELGITGTQASMLFMIAVGRCSTAAELAREYGIDASAVTRLLDRVEKRGLLSRVRSI  99

Query  87   NDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF  144
             D RVV   LT++   +A+          L    EL   FT EE   +   L  +  +
Sbjct  100  EDRRVVRLELTDEGRALAERLPPVFRSVL---DELLGGFTPEEVGFLKSMLRRILSNY  154
```

>**ref|ZP_01131766.1|** transcriptional regulator, MarR family protein [Pseudoalteromonas tunicata D2]
gb|EAR30132.1| transcriptional regulator, MarR family protein [Pseudoalteromonas tunicata D2]
Length=163

Score = 45.8 bits (107), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 29/83 (34%), Positives = 47/83 (56%), Gaps = 1/83 (1%)

```
Query  28   KCESDVKLTSTQEHILMLLAEQISTNAK-IAEKLKISPAAVTKALKKLQEQELIKSSRAT  86
```

```
            K   +  LTS Q  +L  +++Q     K IAE++ +S A +T  L +L+ +EL+   R+T
Sbjct  24   KLSKETGLTSPQLLVLQAISQQDGVMVKEIAEQINLSSATITSILDRLEIRELVIRERST  83

Query  87   NDERVVLWSLTEKAVPVAKEHAT  109
             D+R V  SLT+K   + K+  T
Sbjct  84   TDKRRVGISLTDKGFDIIKDSPT  106


>ref|ZP_00238819.1|  transcriptional regulator, MarR family [Bacillus cereus G9241]
 gb|EAL13614.1|  transcriptional regulator, MarR family [Bacillus cereus G9241]
Length=152

 Score = 45.8 bits (107),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 27/85 (31%), Positives = 49/85 (57%), Gaps = 1/85 (1%)

Query  35   LTSTQEHILMLLAEQISTNA-KIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVL  93
            LT  Q +IL +L    ++ A K+A+K+ + P+A+T  + +L +QEL++      +D RVV+
Sbjct  35   LTPPQFYILKILDHYGASRATKLAKKMYVKPSAITVMIDRLIDQELVERYHDKDDRRVVI  94

Query  94   WSLTEKAVPVAKEHATHHEKTLSTY  118
              LT+K     +E  T   + ++ Y
Sbjct  95   IELTKKGKARVEEAMTARNEHIAKY  119


>ref|YP_002467440.1|  transcriptional regulator, MarR family [Candidatus Methanosphaerula
palustris E1-9c]
 gb|ACL17717.1|  transcriptional regulator, MarR family [Candidatus Methanosphaerula
palustris E1-9c]
Length=159

 GENE ID: 7271351 Mpal_2438 | transcriptional regulator, MarR family
[Candidatus Methanosphaerula palustris E1-9c]

 Score = 45.8 bits (107),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 25/85 (29%), Positives = 47/85 (55%), Gaps = 0/85 (0%)

Query  56   IAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTL  115
            IA+ L ++P+A ++A+ KL  + L+K  R   +ER V   LT++     + H   H++
Sbjct  53   IADLLGVTPSAASQAVTKLAGRGLVKKVRGRKNEREVSLELTDQGWVAYRYHEQTHKEIY  112

Query  116  STYQELGNKFTDEEQEVISKFLSAL  140
            +   E     ++EE E+I++F +A
Sbjct  113  TRTTERVGPLSEEELELIARFFNAF  137


>ref|ZP_03547491.1|  hypothetical protein BLAHAN_01259 [Blautia hansenii DSM 20583]
 gb|EED60137.1|  hypothetical protein BLAHAN_01259 [Blautia hansenii DSM 20583]
Length=168

 Score = 45.4 bits (106),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 32/105 (30%), Positives = 53/105 (50%), Gaps = 4/105 (3%)

Query  41   HILMLLAEQISTN-AKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEK  99
            HI+  + E+ + N + +A+ L ++   +T A+  L ++  +   R+  D RVVL SLT K
Sbjct  60   HIMEAIGEENAKNMSSVAKLLSVTVGTLTIAINGLVKKGYVARERSEEDRRVVLISLTGK  119

Query  100  AVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF  144
                + H   H+  +   Q L     DE+QE++ K L  L E F
Sbjct  120  GRKANEHHKKFHDGMI---QALLKDLDDEQQEILVKSLLNLREFF  161


>ref|ZP_02891041.1|  transcriptional regulator, MarR family [Burkholderia ambifaria
IOP40-10]
 gb|EDT03378.1|  transcriptional regulator, MarR family [Burkholderia ambifaria
IOP40-10]
Length=163

 Score = 45.4 bits (106),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 31/118 (26%), Positives = 59/118 (50%), Gaps = 4/118 (3%)

Query  28   KCESDVKLTSTQEHILMLLA-EQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRAT  86
            + + ++ +T TQ  +L ++A  + ST A++A +  I  +AVT+ L +++++ L+   R+
Sbjct  40   RTQEELGITGTQASMLFMIAVGKCSTAAELAREYGIDASAVTRLLDRVEKRGLLSRVRSI  99

Query  87   NDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF  144
             D RVV   LT++   +A+          L    EL   FT EE   +   L  L  +
Sbjct  100  EDRRVVRLELTDEGRELAERLPPVFRSVL---DELLGGFTPEEVGFLKSMLRRILSNY  154


>ref|YP_001808132.1|  MarR family transcriptional regulator [Burkholderia ambifaria
MC40-6]
 gb|ACB63916.1|  transcriptional regulator, MarR family [Burkholderia ambifaria
MC40-6]
Length=164

 GENE ID: 6177160 BamMC406_1428 | MarR family transcriptional regulator
[Burkholderia ambifaria MC40-6]

 Score = 45.4 bits (106),  Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 31/118 (26%), Positives = 59/118 (50%), Gaps = 4/118 (3%)

Query  28   KCESDVKLTSTQEHILMLLA-EQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRAT  86
            + + ++ +T TQ  +L ++A  + ST A++A +  I  +AVT+ L +++++ L+   R+
Sbjct  40   RTQEELGITGTQASMLFMIAVGKCSTAAELAREYGIDASAVTRLLDRVEKRGLLSRVRSI  99
```

```
Query  87   NDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF  144
            D RVV   LT++   +A+         L    EL   FT EE   +   L  +   +
Sbjct  100  EDRRVVRLELTDEGRALAERLPPVFRSVL---DELLGGFTPEEVGFLKSMLRRILSNY  154
```

>**ref|ZP_02906301.1|** transcriptional regulator, MarR family [Burkholderia ambifaria MEX-5]
gb|EDT42559.1| transcriptional regulator, MarR family [Burkholderia ambifaria MEX-5]
Length=164

Score = 45.4 bits (106), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 31/118 (26%), Positives = 59/118 (50%), Gaps = 4/118 (3%)

```
Query  28   KCESDVKLTSTQEHILMLLA-EQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRAT  86
            + + ++ +T TQ  +L ++A  + ST A++A +  I  +AVT+ L +++++ L+   R+
Sbjct  40   RTQEELGITGTQASMLFMIAVGKCSTAAELAREYGIDASAVTRLLDRVEKRGLLSRVRSI  99

Query  87   NDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF  144
            D RVV   LT++   +A+         L    EL   FT EE   +   L  +   +
Sbjct  100  EDRRVVRLELTDEGRALAERLPPVFRSVL---DELLGGFTPEEVGFLKSMLRRILSNY  154
```

>**ref|ZP_02362996.1|** transcriptional regulator, MarR family protein [Burkholderia oklahomensis C6786]
Length=165

Score = 45.4 bits (106), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 31/126 (24%), Positives = 69/126 (54%), Gaps = 5/126 (3%)

```
Query  6    QIDQFLGTIMQFAEN-KHEILLGKCESDVKLTSTQEHILMLLA-EQISTNAKIAEKLKIS  63
            QI+  +G +M   ++    ++  + ++++ +T TQ  +L +LA  + ST A++A +  I
Sbjct  17   QINDSVGYLMSRVKSLMTNMVTQRTQTELGITGTQATMLFMLAVGKCSTAAELAREYGID  76

Query  64   PAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGN  123
             +A+T+ L +++++ L++  R+ D RVV   LT++   + +         L    ++ +
Sbjct  77   ASAITRLLDRVEKRGLLQRVRSSEDRRVVRLELTDEGRDLTRRMPAIFRSVL---DQVLD  133

Query  124  KFTDEE  129
            FT EE
Sbjct  134  GFTPEE  139
```

>**ref|NP_977055.1|** G MarR family transcriptional regulator [Bacillus cereus ATCC 10987]
gb|AAS39663.1| G transcriptional regulator, MarR family [Bacillus cereus ATCC 10987]
Length=152

GENE ID: 2747926 BCE_0730 | MarR family transcriptional regulator [Bacillus cereus ATCC 10987] (10 or fewer PubMed links)

Score = 45.4 bits (106), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 27/85 (31%), Positives = 49/85 (57%), Gaps = 1/85 (1%)

```
Query  35   LTSTQEHILMLLAEQISTNA-KIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVL  93
            LT  Q +IL +L    ++ A K+A+K+ + P+A+T  + +L +QEL++      +D RVV+
Sbjct  35   LTPPQFYILKILDHYGASRATKLAKKMYVKPSAITVMIDRLIDQELVERYHDKDDRRVVV  94

Query  94   WSLTEKAVPVAKEHATHHEKTLSTY  118
              LT+K     +E  T   + ++ Y
Sbjct  95   IELTKKGKARVEEAMTARNEHIAKY  119
```

>**ref|NP_782475.1|** G MarR family transcriptional regulator [Clostridium tetani E88]
gb|AAO36412.1| G transcriptional regulator, marR family [Clostridium tetani E88]
Length=154

GENE ID: 1058804 marR | MarR family transcriptional regulator [Clostridium tetani E88] (10 or fewer PubMed links)

Score = 45.4 bits (106), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 25/91 (27%), Positives = 50/91 (54%), Gaps = 0/91 (0%)

```
Query  51   STNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATH  110
            +   +IA  L I+ +AV+K +++LQ++ LI SS+  ++++ + ++LT +   + K+H
Sbjct  50   ANGTQIANYLNITRSAVSKIIRRLQKENLIISSQKPDNKKEIFYTLTNEGNNIFKQHKQA  109

Query  111  HEKTLSTYQELGNKFTDEEQEVISKFLSALT  141
             HEK      +   E+E + KFL
Sbjct  110  HEKWEIRDTKFLKTISTNEKETVFKFLKKFN  140
```

>**ref|ZP_03570809.1|** transcriptional regulator, MarR family [Burkholderia multivorans CGD2M]
ref|ZP_03577696.1| transcriptional regulator, MarR family [Burkholderia multivorans CGD2]
ref|ZP_03586132.1| transcriptional regulator, MarR family [Burkholderia multivorans CGD1]
gb|EED99839.1| transcriptional regulator, MarR family [Burkholderia multivorans CGD1]
gb|EEE07966.1| transcriptional regulator, MarR family [Burkholderia multivorans CGD2]
gb|EEE14096.1| transcriptional regulator, MarR family [Burkholderia multivorans CGD2M]
Length=164

```
 Score = 45.1 bits (105),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 32/118 (27%), Positives = 60/118 (50%), Gaps = 4/118 (3%)

Query  28   KCESDVKLTSTQEHILMLLA-EQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRAT  86
            + + ++ +T TQ  +L ++A  + ST A++A +  I  +AVT+ L +++++ L+   R+
Sbjct  40   RTQEELGITGTQASMLFMIAVGKCSTAAELAREYAIDASAVTRLLDRVEKRGLLCRVRSV  99

Query  87   NDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF  144
             D RVV   LT++   +A+         L   Q LG  FT EE   +   L  +   +
Sbjct  100  EDRRVVRLELTDEGRALAERLPAIFRSVLD--QLLGG-FTPEEVGFLKSMLRRILSNY  154


>ref|YP_001119315.1| G MarR family transcriptional regulator [Burkholderia vietnamiensis
G4]
 gb|ABO54480.1| G transcriptional regulator, MarR family [Burkholderia vietnamiensis
G4]
Length=163

 GENE ID: 4953186 Bcep1808_1472 | MarR family transcriptional regulator
[Burkholderia vietnamiensis G4]

 Score = 45.1 bits (105),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 35/126 (27%), Positives = 66/126 (52%), Gaps = 5/126 (3%)

Query  6    QIDQFLGTIMQFAENKHEILLG-KCESDVKLTSTQEHILMLLA-EQISTNAKIAEKLKIS  63
            QI+  +G +M   ++    L+  + + ++ +T TQ  +L ++A  + ST A++A +  I
Sbjct  17   QINDSVGYLMSRVKSVMTNLVTQRTQEELGITGTQASMLFMIAVGKCSTAAELAREYGID  76

Query  64   PAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGN  123
             +AVT+ L +++++ L+   R+  D RVV   LT++   +A+         L    EL
Sbjct  77   ASAVTRLLDRVEKRGLLSRVRSIEDRRVVRLELTDEGRALAERLPPVFRSVL---DELLE  133

Query  124  KFTDEE  129
             FT EE
Sbjct  134  GFTPEE  139


>ref|YP_002418276.1| G Histone acetyltransferase HPA2 and related acetyltransferases
[Vibrio splendidus LGP32]
 emb|CAV19992.1| G Histone acetyltransferase HPA2 and related acetyltransferases
[Vibrio splendidus LGP32]
Length=301

 GENE ID: 7162224 VS_2735 | Histone acetyltransferase HPA2 and related
acetyltransferases [Vibrio splendidus LGP32]

 Score = 45.1 bits (105),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 35/117 (29%), Positives = 60/117 (51%), Gaps = 1/117 (0%)

Query  25   LLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSR  84
            +L K  D+ L   Q H L+ L +Q  T  ++A+KL I  +  ++A+  L +  LI++S
Sbjct  19   MLDKDCGDIALPPIQAHTLIELEQQPLTVNQLADKLNIDKSNASRAVNNLAKNSLIQTSP  78

Query  85   ATNDERVVLWSLTEKA-VPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSAL  140
              ND+R V+ S+T++    +AK H   ++   S  + L    T +    I  +L AL
Sbjct  79   HPNDKRSVVASVTDQGKNTLAKLHNQQNQFYDSVLEHLTEAETQQVSGGIEHYLKAL  135


>ref|ZP_02355848.1|  transcriptional regulator, MarR family protein [Burkholderia
oklahomensis EO147]
Length=165

 Score = 45.1 bits (105),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 31/126 (24%), Positives = 69/126 (54%), Gaps = 5/126 (3%)

Query  6    QIDQFLGTIMQFAEN-KHEILLGKCESDVKLTSTQEHILMLLA-EQISTNAKIAEKLKIS  63
            QI+  +G +M   ++    ++  + ++++ +T TQ  +L +LA  + ST A++A +  I
Sbjct  17   QINDSVGYLMSRVKSLMTNMVTQRTQTELGITGTQATMLFMLAVGKCSTAAELAREYGID  76

Query  64   PAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGN  123
             +A+T+ L +++++ L+   R+  D RVV   LT++   +A+         L    EL
Sbjct  77   ASAITRLLDRVEKRGLLQRVRSSEDRRVVRLELTDEGRELTRRMPAIFRSVL---DQVLD  133

Query  124  KFTDEE  129
             FT EE
Sbjct  134  GFTPEE  139


>ref|YP_443075.1| G MarR family transcriptional regulator [Burkholderia thailandensis
E264]
 ref|ZP_02374954.1|  transcriptional regulator, MarR family protein [Burkholderia
thailandensis TXDOH]
 ref|ZP_02388872.1|  transcriptional regulator, MarR family protein [Burkholderia
thailandensis Bt4]
 gb|ABC39239.1| G transcriptional regulator, MarR family [Burkholderia thailandensis
E264]
Length=165

 GENE ID: 3849294 BTH_I2558 | MarR family transcriptional regulator
[Burkholderia thailandensis E264] (10 or fewer PubMed links)

 Score = 44.7 bits (104),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 33/126 (26%), Positives = 67/126 (53%), Gaps = 5/126 (3%)
```

Annex 1

```
Query  6    QIDQFLGTIMQFAEN-KHEILLGKCESDVKLTSTQEHILMLLA-EQISTNAKIAEKLKIS  63
            QI+  +G +M   ++    ++  + ++++ +T TQ  +L +LA  + ST A++A +  I
Sbjct  17   QINDSVGYLMSRVKSLMTNMVTQRTQTELGITGTQATMLFMLAVGKCSTAAELAREYGID  76

Query  64   PAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGN  123
             +A+T+ L +++++ L++  R++ D RVV   LT++   + K          L    E
Sbjct  77   ASAITRLLDRVEKRGLLQRVRSSEDRRVVRLELTDEGRELTKRMPEIFRSVLDQVLE---  133

Query  124  KFTDEE  129
             FT EE
Sbjct  134  GFTPEE  139


>ref|ZP_02633998.1|  transcriptional regulator, MarR family [Clostridium perfringens
E str. JGS1987]
 ref|ZP_02636384.1|  transcriptional regulator, MarR family [Clostridium perfringens
B str. ATCC 3626]
 ref|ZP_02643088.1|  transcriptional regulator, MarR family [Clostridium perfringens
NCTC 8239]
 7 more sequence titles

ref|ZP_02629009.2|  transcriptional regulator, MarR family [Clostridium perfringens
C str. JGS1495]
 ref|ZP_02954000.1|  transcriptional regulator, MarR family [Clostridium perfringens
D str. JGS1721]
 gb|EDS81585.1|  transcriptional regulator, MarR family [Clostridium perfringens
C str. JGS1495]
 gb|EDT13394.1|  transcriptional regulator, MarR family [Clostridium perfringens
E str. JGS1987]
 gb|EDT23419.1|  transcriptional regulator, MarR family [Clostridium perfringens
B str. ATCC 3626]
 gb|EDT71039.1|  transcriptional regulator, MarR family [Clostridium perfringens
D str. JGS1721]
 gb|EDT77904.1|  transcriptional regulator, MarR family [Clostridium perfringens
NCTC 8239]
Length=154

 Score = 44.7 bits (104),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 33/99 (33%), Positives = 50/99 (50%), Gaps = 5/99 (5%)

Query  48   EQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEH  107
            E+  T +++A  LKI+   +T A+ KL ++  +   R   D RVV+  LTEK     K H
Sbjct  49   EKARTMSEVALDLKITVGTLTTAINKLIKKGYVNRRRIEEDRRVVMIELTEKGTLAYKVH  108

Query  108  ATHHEKTLS-TYQELGNKFTDEEQEVISKFLSALTEEFQ  145
             HE+ +    +ELG      E+EV+   L  L + FQ
Sbjct  109  EKFHEEMIDHVLEELGVS----EEEVLISSLDKLDKFFQ  143


>ref|YP_001374721.1|  MarR family transcriptional regulator [Bacillus cereus subsp.
cytotoxis NVH 391-98]
 gb|ABS21726.1|  transcriptional regulator, MarR family [Bacillus cereus subsp.
cytotoxis NVH 391-98]
Length=136

 GENE ID: 5344927 Bcer98_1405 | MarR family transcriptional regulator
[Bacillus cereus subsp. cytotoxis NVH 391-98]

 Score = 44.7 bits (104),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 37/119 (31%), Positives = 62/119 (52%), Gaps = 4/119 (3%)

Query  28   KCESDVKLTSTQEHILMLLAEQISTN-AKIAEKLKISPAAVTKALKKLQEQELIKSSRAT  86
            +CE +  L+     IL + + +  T  +KIA +L +S    ++ +K+L +++LI   R
Sbjct  16   RCEYENNLSHQAIRILQITSREAETTISKIASELNLSHNTASEHVKRLIQKDLILKERNK  75

Query  87   NDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEFQ  145
             DERVV  +LT K      +H    EK L     L ++ + EEQ++I +  S L +E Q
Sbjct  76   KDERVVNLALTAKGKEALIKHTLLDEKKLKI---LESQLSKEEQQIIEQAFSILAKEAQ  131


>ref|YP_819461.1|  transcriptional regulator [Leuconostoc mesenteroides subsp. mesenteroides
ATCC 8293]
 gb|ABJ63088.1|  Transcriptional regulator [Leuconostoc mesenteroides subsp. mesenteroides
ATCC 8293]
Length=146

 GENE ID: 4423731 LEUM_2018 | transcriptional regulator
[Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293]
(10 or fewer PubMed links)

 Score = 44.7 bits (104),  Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 30/84 (35%), Positives = 46/84 (54%), Gaps = 5/84 (5%)

Query  34   KLTSTQEHILMLL-AEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVV  92
            K+ STQ H+LMLL   Q  TN ++A  + +S  A+TKA+K L     + +  +D+R
Sbjct  32   KINSTQAHLLMLLKILQSQTNTELAAAMNLSKPAITKAIKNLMRYHYVIAVVDDSDKRST  91

Query  93   LWSLTEKAVPVA----KEHATHHE  112
             + LTE    +A    + HAT H+
Sbjct  92   HYLLTEDGEKLAQLHEQAHATMHD  115


>ref|ZP_02027443.1|  hypothetical protein EUBVEN_02713 [Eubacterium ventriosum ATCC
27560]
```

Annex 1

gb|EDM50067.1| hypothetical protein EUBVEN_02713 [Eubacterium ventriosum ATCC 27560]
Length=151

Score = 44.7 bits (104), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 27/90 (30%), Positives = 53/90 (58%), Gaps = 3/90 (3%)

```
Query  56   IAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTL  115
            IA+K+KI+  ++T ++  L ++  ++ +R+  D R+V  +LTEK +   K H   HEK
Sbjct  60   IAKKMKITVGSLTTSMNSLVKKHYVERNRSEEDRRIVNITLTEKGIKAYKHHEEFHEK--  117

Query  116  STYQELGNKFTDEEQEVISKFLSALTEEFQ  145
               Q   ++ +++E +V+ K L+ L++ F
Sbjct  118  -MSQAAISEMSEDEVKVLLKSLNNLSKFFH  146
```

Select All Get selected sequences Distance tree of results

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THE NATH LAW GROUP
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ETATS-UNIS D'AMERIQUE

Attention : M. William E. BEAUMONT

Paris, March 5, 2009

UNITED STATES OF AMERICA - PATENT APPLICATION No. 10/525,449
filed on : August 29, 2003
In the name of: INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE.
For : « Zinc-regulated prokaryotic expression cassettes. »
Invention : POQUET Isabelle, LLULL Daniel

Y/Ref.: 1169-034 O/Ref.: MJP/DG/md - F053900116/US/PCT

Dear Sir,

We refer to your letter of October 31, 2008 transmitting us the 1st Office Action issued in relation with the above-referred application.

We have discussed this case with the applicant, and beg you to find herein enclosed our comments and instructions concerning this application.

Since we believe that an interview with the Examiner will be necessary in order to discuss the objections and the possible amendments to the claims, you may request a third month extension of time.

Please **acknowledge receipt** of this letter by return.

In the meantime, we are,

Very truly yours,

M.J. VIALLE-PRESLES **B. ORES**

Encl. : - Memorandum, and
- Annexes (only by e-mail).

U.S Application 10/1525449

MEMORANDUM OF INSTRUCTIONS FOR RESPONDING THE OFFICE ACTION OF OCTOBER 7, 2008

1) Claims objections:

We beg you to amend the claims as requested by the Examiner. Concerning claim 15, it differs from claim 12 in that the expression cassette does not comprise the sequence encoding the ZitR repressor (cf § [0025] to [0027] of the instant application), and can be used to obtain constitutive expression of a protein of interest in bacterial strains wherein the endogenous ZitR repressor is inactivated (cf. § [0053] of the instant application)

2) Rejection under 35 USC § 112.

We wish to point out that the definition "at least 80% identity with the *Lactococcus lactis* ZitR protein GENBANK AAK06214" does not encompass a broad variety of proteins.

The results of BLAST searchs using GENBANK AAK06214 as a query are enclosed therein. A first search was performed against all the protein sequences available in the nr database (all known protein sequences, including the complete sequences of various bacteria). The enclosed results (Annex 1) show that the only proteins having more than 80% identity with GENBANK AAK06214 (which is the ZitR protein of *Lactococcus lactis* subsp. *lactis* Il1403), are the ZitR proteins of *Lactococcus lactis* subsp. *cremoris* SK11 (89% identity) and the ZitR proteins of *Lactococcus lactis* subsp. *cremoris* MG1363 (88% identity).

A second search was performed against the whole genome sequences of *Lactococcus lactis* subsp. *lactis* Il1403, *Lactococcus lactis* subsp. *cremoris* SK11 and *Lactococcus lactis* subsp. *cremoris* MG1363. The enclosed results (Annex 2) show that the only lactococcal proteins having more than 80% identity with GENBANK AAK06214, are the ZitR proteins of *Lactococcus lactis* subsp. *cremoris* SK11 (89% identity) and the ZitR proteins of *Lactococcus lactis* subsp. *cremoris* MG1363 (88% identity).

Therefore, obtaining a nucleotide sequence encoding a protein having more than 80% identity with GENBANK AAK06214 would not have required require undue experimentation for one of skill in the art. He would have easily obtained it by routine screening of a lactococcal DNA library with a probe derived from the nucleotide sequence encoding GENBANK AAK06214 (or from nucleotides 357-794 of SEQ ID NO:2), and would inevitably have found the orthologs of GENBANK AAK06214.

We beg you to request an interview with the Examiner in order to discuss this issue of enablement. If necessary, you may amend paragraph b) of claim 12 so as to

specify that the polypeptide is a lactococcal polypeptide, and/or to indicate a higher percent of identity (85% rather than 80%) with GENBANK AAK06214.

3) Rejection under 35 USC § 102.

We beg you to insert in claims 12 and 15 the same disclaimer as in claim 18, which excludes the cassette and vector of POQUET et al.

Annex 2

BLAST Basic Local Alignment Search Tool

Formatting options Download

gb|AAK06214| (145 letters)

Results for: gb|AAK06214.1 zinc transport transcriptional regulator [Lactococcus lactis subsp. lactis Il1403](145aa)
Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID
gi|12725171|gb|AAK06214.1|AE006439_11
Description
zinc transport transcriptional regulator [Lactococcus lactis subsp. lactis Il1403]
Molecule type
amino acid
Query Length
145

Database Name
3 databases
Description
Program
BLASTP 2.2.19+ Citation

Reference
Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.
Reference - compositional score matrix adjustment
Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.
Other reports: Search Summary [Taxonomy reports] [Distance tree of results]

Search Parameters

Program	blastp
Word size	3
Expect value	10
Hitlist size	100
Gapcosts	11,1
Matrix	BLOSUM62
Threshold	11
Composition-based stats	2
Low Complexity Filter	Yes
Filter string	L;
Genetic Code	1
Window Size	40

Database

Posted date	Mar 2, 2009 5:57 PM
Number of letters	2,055,736
Number of sequences	7,259
Entrez query	none

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.310848	0.267
K	0.124161	0.041

H 0.32399 0.14

Results Statistics

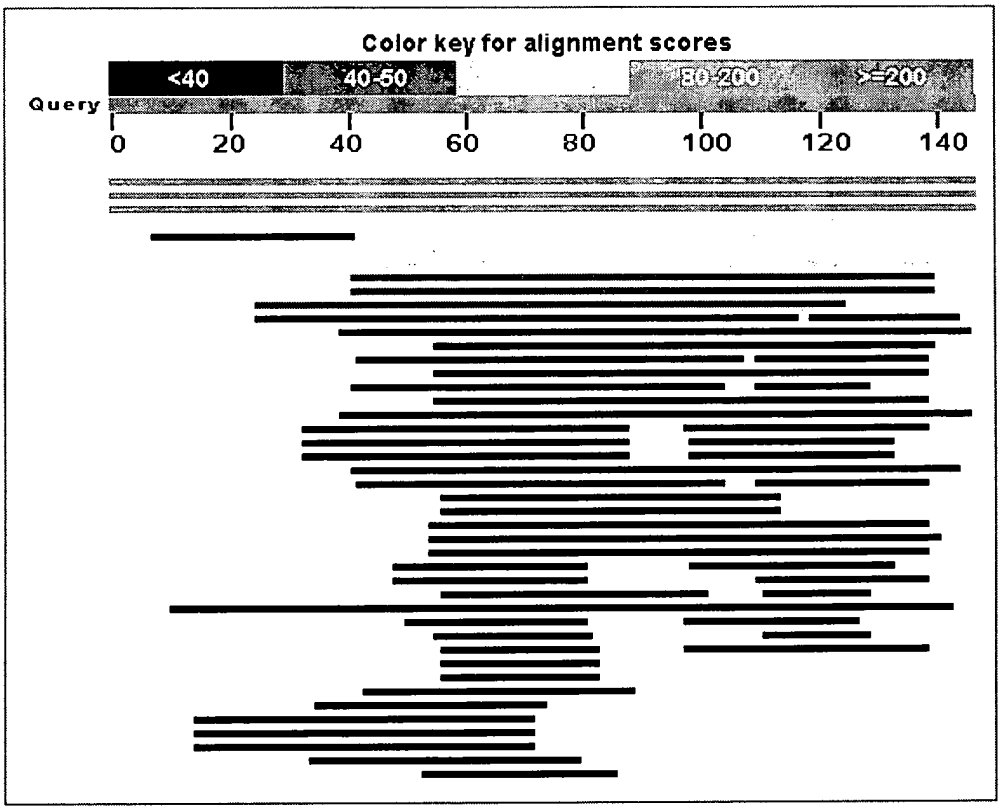
Length adjustment	78
Effective length of query	67
Effective length of database	1489534
Effective search space	99798778
Effective search space used	99798778

Graphic Summary

Distribution of 58 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



Annex 2

Descriptions

Sequences producing significant alignments:	Score (Bits)	E Value	
ref|NP_268273.1| zinc transport transcription regulator [Lact...	291	2e-80	G
ref|YP_811979.1| transcriptional regulator [Lactococcus lacti...	268	2e-73	G
ref|YP_001033643.1| transcriptional regulator of the zit oper...	267	3e-73	G
ref|YP_001033431.1| MarR family transcriptional regulator [La...	53.9	6e-09	G
ref|YP_808725.1| transcriptional regulator [Lactococcus lacti...	51.2	4e-08	G
ref|NP_266864.1| transcription regulator [Lactococcus lactis ...	51.2	4e-08	G
ref|YP_808147.1| transcriptional regulator [Lactococcus lacti...	50.4	7e-08	G
ref|YP_001031482.1| MarR family transcriptional regulator [La...	49.3	1e-07	G
ref|NP_266269.1| transcription regulator [Lactococcus lactis ...	46.1	1e-06	G
ref|NP_267626.1| transcription regulator [Lactococcus lactis ...	41.2	4e-05	G
ref|YP_001033744.1| MarR family transcriptional regulator [La...	38.5	2e-04	G
ref|YP_808479.1| transcriptional regulator [Lactococcus lacti...	37.4	9e-04	G
ref|NP_266463.1| MarR family transcriptional regulator [Lacto...	36.2	0.001	G
ref|NP_266747.1| transcription regulator [Lactococcus lactis ...	35.8	0.002	G
ref|YP_001031687.1| MarR family transcriptional regulator [La...	35.4	0.002	G
ref|NP_266818.1| MarR family transcriptional regulator [Lacto...	35.4	0.002	G
ref|YP_808737.1| MarR family transcriptional regulator [Lacto...	35.4	0.002	G
ref|YP_001031731.1| transcriptional regulator [Lactococcus la...	34.7	0.003	G
ref|YP_001031879.1| putative transcriptional regulator [Lacto...	32.3	0.017	G
ref|YP_808573.1| BadM/Rrf2 family transcriptional regulator [...	32.3	0.018	G
ref|NP_266714.1| hypothetical protein L153086 [Lactococcus la...	32.3	0.018	G
ref|YP_001033090.1| MarR family transcriptional regulator [La...	31.6	0.031	G
ref|YP_808765.1| MarR family transcriptional regulator [Lacto...	31.6	0.034	G
ref|YP_808795.1| MarR family transcriptional regulator [Lacto...	31.2	0.044	G
ref|NP_266926.1| MarR family transcriptional regulator [Lacto...	31.2	0.045	G
ref|YP_001032909.1| MarR family transcriptional regulator [La...	28.9	0.18	G
ref|YP_001032520.1| MarR family transcriptional regulator [La...	28.1	0.31	G
ref|NP_267064.1| transcription regulator [Lactococcus lactis ...	28.1	0.35	G
ref|YP_001032533.1| transcriptional regulator [Lactococcus la...	28.1	0.38	G
ref|YP_809512.1| Mn-dependent transcriptional regulator [Lact...	28.1	0.38	G
ref|NP_267461.1| transcription regulator [Lactococcus lactis ...	27.7	0.42	G
ref|NP_267696.1| transcription regulator [Lactococcus lactis ...	27.3	0.61	G
ref|NP_266753.1| NADPH-flavin oxidoreductase [Lactococcus lac...	27.3	0.67	G
ref|NP_267412.1| metalloregulator [Lactococcus lactis subsp. ...	26.6	1.1	G
ref|YP_001031697.1| putative cobalt ABC transporter ATP-bindi...	26.2	1.2	G
ref|NP_266673.1| quinone oxidoreductase [Lactococcus lactis s...	25.4	2.4	G
ref|NP_268402.1| alkylphosphonate uptake protein [Lactococcus...	25.4	2.4	G
ref|YP_808209.1| transcriptional repressor CodY [Lactococcus ...	24.6	3.4	G
ref|YP_001031533.1| transcriptional repressor CodY [Lactococc...	24.6	3.4	G
ref|NP_266317.1| transcriptional repressor CodY [Lactococcus ...	24.6	3.5	G
ref|NP_266838.1| intercellular adhesion protein [Lactococcus ...	24.6	3.6	G
ref|NP_266710.1| transcription regulator [Lactococcus lactis ...	24.6	3.6	G
ref|NP_266438.1| amino acid amidohydrolase [Lactococcus lacti...	24.6	4.1	G
ref|YP_808446.1| lysyl-tRNA synthetase [Lactococcus lactis su...	24.6	4.3	G
ref|YP_001031741.1| lysyl-tRNA synthetase [Lactococcus lactis...	24.3	4.7	G
ref|NP_266529.1| lysyl-tRNA synthetase [Lactococcus lactis su...	24.3	4.7	G
ref|YP_001031937.1| NADPH-flavin oxidoreductase [Lactococcus ...	24.3	5.2	G
ref|YP_809603.1| NADPH-flavin oxidoreductase [Lactococcus lac...	24.3	5.5	G
ref|NP_268193.1| exported serine protease [Lactococcus lactis...	23.9	6.1	G
ref|YP_001033660.1| housekeeping protease [Lactococcus lactis...	23.9	6.5	G
ref|YP_811995.1| trypsin-like serine protease [Lactococcus la...	23.9	6.6	G
ref|NP_268332.1| hypothetical protein L35545 [Lactococcus lac...	23.5	7.5	G

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ref|NP_268337.1|	hypothetical protein L39650 [Lactococcus lac...	23.5	7.7	G
ref|YP_001032772.1|	superfamily II DNA/RNA helicase [Lactococ...	23.5	7.8	G
ref|YP_001033122.1|	quinone oxidoreductase [Lactococcus lacti...	23.5	9.3	G
ref|YP_808733.1|	quinone oxidoreductase [Lactococcus lactis s...	23.5	9.3	G
ref|YP_796521.1|	hypothetical protein LACR_C57 [Lactococcus l...	23.5	9.5	G
ref|YP_812045.1|	hypothetical protein LACR_2554 [Lactococcus ...	23.1	10.0	G

Alignments Select All Get selected sequences Distance tree of results

>ref|NP_268273.1| G zinc transport transcription regulator [Lactococcus lactis subsp. lactis Il1403]
Length=145

GENE ID: 1115793 zitR | zinc transport transcription regulator [Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 291 bits (744), Expect = 2e-80, Method: Compositional matrix adjust.
Identities = 145/145 (100%), Positives = 145/145 (100%), Gaps = 0/145 (0%)

```
Query  1    MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL  60
            MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL
Sbjct  1    MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL  60

Query  61   KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE  120
            KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE
Sbjct  61   KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE  120

Query  121  LGNKFTDEEQEVISKFLSALTEEFQ  145
            LGNKFTDEEQEVISKFLSALTEEFQ
Sbjct  121  LGNKFTDEEQEVISKFLSALTEEFQ  145
```

>ref|YP_811979.1| G transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
Length=145

GENE ID: 4433026 LACR_2420 | transcriptional regulator [Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 268 bits (685), Expect = 2e-73, Method: Compositional matrix adjust.
Identities = 130/145 (89%), Positives = 141/145 (97%), Gaps = 0/145 (0%)

```
Query  1    MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL  60
            MSLANQIDQFLG IMQFAENKHEILLG+CES+VKLTSTQEHILM+LA ++STNA+IAE+L
Sbjct  1    MSLANQIDQFLGAIMQFAENKHEILLGECESNVKLTSTQEHILMILAAEVSTNARIAEQL  60

Query  61   KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE  120
            KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHA HHEKTLSTYQE
Sbjct  61   KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHAAHHEKTLSTYQE  120

Query  121  LGNKFTDEEQEVISKFLSALTEEFQ  145
            LG+KFTDEEQ+VIS+FLS LTEEF+
Sbjct  121  LGDKFTDEEQKVISQFLSVLTEEFR  145
```

>ref|YP_001033643.1| G transcriptional regulator of the zit operon [Lactococcus lactis subsp. cremoris MG1363]
Length=145

GENE ID: 4799067 zitR | transcriptional regulator of the zit operon [Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 267 bits (682), Expect = 3e-73, Method: Compositional matrix adjust.
Identities = 129/145 (88%), Positives = 141/145 (97%), Gaps = 0/145 (0%)

```
Query  1    MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL  60
            MSLANQIDQFLG IMQFAENKHEILLG+CES+VKLTSTQEHILM+LA ++STNA+IAE+L
Sbjct  1    MSLANQIDQFLGAIMQFAENKHEILLGECESNVKLTSTQEHILMILAAEVSTNARIAEQL  60

Query  61   KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE  120
            KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKA+PVAKEHA HHEKTLSTYQE
Sbjct  61   KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAIPVAKEHAAHHEKTLSTYQE  120

Query  121  LGNKFTDEEQEVISKFLSALTEEFQ  145
            LG+KFTDEEQ+VIS+FLS LTEEF+
Sbjct  121  LGDKFTDEEQKVISQFLSVLTEEFR  145
```

>ref|YP_001033131.1| G MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]
Length=295

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GENE ID: 4797387 rmaB | MarR family transcriptional regulator
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 53.9 bits (128), Expect = 6e-09, Method: Compositional matrix adjust.
Identities = 38/101 (37%), Positives = 54/101 (53%), Gaps = 3/101 (2%)

```
Query  42   ILMLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAV  101
            ++ L  E   TNA+IAE L I P++VT  +K+L+E E++   +  ND+RV    LTEK
Sbjct  47   LVELWNEDGLTNAEIAELLDIKPSSVTTQVKQLEEAEMVIRKQDENDKRVNRIFLTEKGR  106

Query  102  PVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTE  142
               +   T H     T    GN  TDEEQE ++  +  L E
Sbjct  107  EAQETRDTMHNDISETI--FGN-LTDEEQEQLANLMEKLVE  144
```

>ref|YP_808725.1| transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
Length=292

GENE ID: 4432217 LACR_0742 | transcriptional regulator
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 51.2 bits (121), Expect = 4e-08, Method: Compositional matrix adjust.
Identities = 35/91 (38%), Positives = 50/91 (54%), Gaps = 3/91 (3%)

```
Query  52   TNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHH  111
            TNA+IAE L I P++VT  +K+L+E E++   +  ND+RV    LTEK     +   T H
Sbjct  57   TNAEIAELLDIKPSSVTAQVKQLEEAEMVIRKQDENDKRVNRIFLTEKGREAQETRDTMH  116

Query  112  EKTLSTYQELGNKFTDEEQEVISKFLSALTE  142
                T    GN  TDEEQ+ ++  +  L E
Sbjct  117  NDISETI--FGN-LTDEEQKQLANLMEKLVE  144
```

>ref|NP_266864.1| transcription regulator [Lactococcus lactis subsp. lactis Il1403]
Length=291

GENE ID: 1114333 rmaB | transcription regulator
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 51.2 bits (121), Expect = 4e-08, Method: Compositional matrix adjust.
Identities = 35/91 (38%), Positives = 50/91 (54%), Gaps = 3/91 (3%)

```
Query  52   TNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHH  111
            TNA+IAE L I P++VT  +K+L+E E++   +  ND+RV    LT+K     +   T H
Sbjct  57   TNAEIAELLDIKPSSVTAQVKQLEEAEMVIRKQDENDKRVSRIFLTDKGREAQETRDTMH  116

Query  112  EKTLSTYQELGNKFTDEEQEVISKFLSALTE  142
                T    GN  TDEEQE ++  +  L E
Sbjct  117  NDISETI--FGN-LTDEEQEQLAFLMEKLVE  144
```

>ref|YP_808147.1| transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
Length=169

GENE ID: 4432499 LACR_0099 | transcriptional regulator
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 50.4 bits (119), Expect = 7e-08, Method: Compositional matrix adjust.
Identities = 27/98 (27%), Positives = 55/98 (56%), Gaps = 0/98 (0%)

```
Query  41   HILMLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKA  100
            HIL  L ++  T  ++A KL ++   VT+A++ L + + + + +A ND++ + + +T K
Sbjct  53   HILSALTKKDLTGIELATKLSVTRGGVTRAVQNLIKHQFLTTYQADNDKKKIYYHITTKG  112

Query  101  VPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLS  138
            + VA  H   H+       ++ +K+ + E+ +I  FLS
Sbjct  113  LKVASIHDKMHKIMDLKLGQIFDKYNENEKSIILNFLS  150
```

>ref|YP_001031482.1| MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]
Length=172

GENE ID: 4798609 rmaD | MarR family transcriptional regulator
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 49.3 bits (116), Expect = 1e-07, Method: Compositional matrix adjust.
Identities = 26/98 (26%), Positives = 55/98 (56%), Gaps = 0/98 (0%)

```
Query  41   HILMLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKA  100
            HIL  L ++  T  ++A KL ++   VT+A++ L + + + + +A ND++ + + +T K
Sbjct  56   HILSALTKKDLTGIELATKLSVTRGGVTRAVQNLIKHQFLTTYQADNDKKKIYYHITTKG  115

Query  101  VPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLS  138
            + VA  H   H+       ++ +K+ + E+ +I  FLS
Sbjct  116  LKVASIHDKMHKIMDLKLGQIFDKYNENDKSIILNFLS  153
```

>**ref|NP_266269.1|** transcription regulator [Lactococcus lactis subsp. lactis Il1403]
Length=163

GENE ID: 1113719 rmaD | transcription regulator
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 46.2 bits (108), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 26/98 (26%), Positives = 55/98 (56%), Gaps = 0/98 (0%)

```
Query  41   HILMLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKA  100
            HIL  L ++  T  ++A KL ++   VT+A++ L + + + + ++ +D++ + + LT K
Sbjct  53   HILSALTKEDLTGIELATKLSVTRGGVTRAVQNLIKYQFLTTYQSESDKKKIFYHLTVKG  112

Query  101  VPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLS  138
              VA  H    H+        ++ +K+ ++E+ +I  FLS
Sbjct  113  RKVATIHDKMHKIMDIRLGQIFDKYNEQEKSIILSFLS  150
```

>**ref|NP_267628.1|** transcription regulator [Lactococcus lactis subsp. lactis Il1403]
Length=356

GENE ID: 1115129 rmaC | transcription regulator
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 41.2 bits (95), Expect = 4e-05, Method: Compositional matrix adjust.
Identities = 29/100 (29%), Positives = 52/100 (52%), Gaps = 1/100 (1%)

```
Query  25   LLGKCESDVKLTSTQEHILMLL-AEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSS  83
            +  K E     + T+  ++M+L  +   + +++  +LKI  AAVT+ LK L+E+ L+K
Sbjct  20   MTAKFEKSTGYSITRYQLMMILKCKGRCSQSQLQNELKIDSAAVTRHLKLLEEKNLVKRE  79

Query  84   RATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGN  123
            R   + R V   +T+KA       A  H+ +L   Q++ N
Sbjct  80   RNKENNREVFVEITDKAKNDLALCAKKHDDSLDESQQILN  119
```

>**ref|YP_001032345.1|** MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]
Length=139

GENE ID: 4798214 rmaC | MarR family transcriptional regulator
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 38.9 bits (89), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 25/92 (27%), Positives = 49/92 (53%), Gaps = 1/92 (1%)

```
Query  25   LLGKCESDVKLTSTQEHILMLL-AEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSS  83
            +  K E     + T+  ++M+L  +   +  ++  +LKI  AAVT+ LK L+E+ L+K
Sbjct  20   MTAKFEKSTGFSITRYQLMMILKCKGRCSQTQLQNELKIDSAAVTRHLKLLEEKNLVKRQ  79

Query  84   RATNDERVVLWSLTEKAVPVAKEHATHHEKTL  115
            R  ++ R V   +T++A    +  A  H+ ++
Sbjct  80   RNKDNNREVFVEITDEAKADLERCAREHDNSV  111
```

>**ref|YP_808479.1|** transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
Length=166

GENE ID: 4433047 LACR_0453 | transcriptional regulator
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 37.0 bits (84), Expect = 9e-04, Method: Compositional matrix adjust.
Identities = 31/111 (27%), Positives = 54/111 (48%), Gaps = 13/111 (11%)

```
Query  39   QEHILMLLAEQISTNAKIAEK-----LKISPAAVTKALKKLQEQELIKSSRATNDERVVL  93
            Q  IL +L E     N+K+ +K     L + P + ++ +KKL++++ I    +   D+R  +
Sbjct  43   QGQILNILME----NSKMTQKNLVAQLDMRPQSASEMIKKLEKKQFISRQKDAQDKRGFI  98

Query  94   WSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF  144
              SLTEK   V +E A   E         +   FT+EE+   ++ +  L  E
Sbjct  99   ISLTEKGKAVLEESAEQTELVPG----IMTSFTEEEKIEFARLIGKLQSEL  145
```

>**ref|NP_266463.1|** MarR family transcriptional regulator [Lactococcus lactis subsp. lactis Il1403]
Length=159

GENE ID: 1113917 napB | MarR family transcriptional regulator
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 36.2 bits (82), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 23/84 (27%), Positives = 46/84 (54%), Gaps = 0/84 (0%)

```
Query  55   KIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKT  114
```

```
            K+A  L ++  A +K  KKL ++ L++S +   +++ + + LT++   +   H + H+K
Sbjct  60   KLAHHLYMTRGAASKIAKKLLKKNLVESYQIPQNKKEIYFRLTKEGQEINDRHESLHQKF  119

Query  115  LSTYQELGNKFTDEEQEVISKFLS  138
             Q + ++ TDE    I KFL+
Sbjct  120  SEKDQVIFDELTDESVSNILKFLN  143
```

>**ref|NP_266747.1|** transcription regulator [Lactococcus lactis subsp. lactis Il1403]
Length=143

GENE ID: 1114211 rmaJ | transcription regulator
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 35.8 bits (81), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 23/65 (35%), Positives = 33/65 (50%), Gaps = 0/65 (0%)

```
Query  42   ILMLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAV  101
            I ML  E   T  K+ E+L +    ++  LK+L+ +  I   R+  DER V   LT+K
Sbjct  40   IAMLAIENKMTINKLGEELSLDSGTLSPLLKRLEAKGYIVRKRSDKDERSVELFLTDKGA  99

Query  102  PVAKE  106
             V KE
Sbjct  100  QVKKE  104
```

>**ref|YP_001031675.1|** MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]
Length=157

GENE ID: 4798013 napB | MarR family transcriptional regulator
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 35.4 bits (80), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 23/83 (27%), Positives = 45/83 (54%), Gaps = 0/83 (0%)

```
Query  55   KIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKT  114
            K+A  L ++  A +K  KKL ++ LI+S +   +++ + + LT++   +   H + H+K
Sbjct  58   KLAHHLYMTRGAASKIAKKLLKKNLIESYQIPQNKKEIYFRLTKEGQQINDRHESLHQKF  117

Query  115  LSTYQELGNKFTDEEQEVISKFL  137
             Q + ++ TDE    I +FL
Sbjct  118  SQNDQVIFDELTDEAVSNILEFL  140
```

>**ref|NP_266898.1|** MarR family transcriptional regulator [Lactococcus lactis subsp. lactis Il1403]
Length=158

GENE ID: 1114368 rmaA | MarR family transcriptional regulator
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 35.4 bits (80), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 22/66 (33%), Positives = 36/66 (54%), Gaps = 3/66 (4%)

```
Query  41   HILMLLAEQISTNA---KIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLT  97
             +L L++  I  N    +I + L I  ++V +A+K L E+E +   R   D+RV   SLT
Sbjct  42   QLLCLISLYIKDNQSQEQITDDLSIDKSSVHRAIKGLIEKEYVSRVRDEKDKRVYRVSLT  101

Query  98   EKAVPV  103
            +KA  +
Sbjct  102  QKARDI  107
```

>**ref|YP_808372.1|** MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
Length=157

GENE ID: 4434175 LACR_0343 | MarR family transcriptional regulator
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 35.4 bits (80), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 23/83 (27%), Positives = 45/83 (54%), Gaps = 0/83 (0%)

```
Query  55   KIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKT  114
            K+A  L ++  A +K  KKL ++ LI+S +   +++ + + LT++   +   H + H+K
Sbjct  58   KLAHHLYMTRGAASKIAKKLLKKNLIESYQIPQNKKEIYFRLTKEGQQINDRHESLHQKF  117

Query  115  LSTYQELGNKFTDEEQEVISKFL  137
             Q + ++ TDE    I +FL
Sbjct  118  SQNDQVIFDELTDEAVSNILEFL  140
```

>**ref|YP_001031774.1|** transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]
Length=166

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GENE ID: 4798362 llmg_0424 | transcriptional regulator
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 35.0 bits (79), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 29/111 (26%), Positives = 53/111 (47%), Gaps = 13/111 (11%)

```
Query  39   QEHILMLLAEQISTNAKIAEK-----LKISPAAVTKALKKLQEQELIKSSRATNDERVVL  93
            Q  IL +L E    N+K+ +K     L + P + ++ +KKL++++ I   +   D+R  +
Sbjct  43   QGQILNILME----NSKMTQKNLVAQLDMRPQSASEMIKKLEKKQFISRQKDAQDKRGFI  98

Query  94   WSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF  144
             SLTEK   V +E      +       +   FT+EE+   ++ +  L  E
Sbjct  99   ISLTEKGKAVLEESTEQTGRVPG----IMTSFTEEEKIEFARLIGKLQSEL  145
```

>**ref|YP_001031879.1|** putative transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]
Length=156

GENE ID: 4796958 llmg_0529 | putative transcriptional regulator
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 32.3 bits (72), Expect = 0.017, Method: Compositional matrix adjust.
Identities = 18/62 (29%), Positives = 38/62 (61%), Gaps = 7/62 (11%)

```
Query  33  VKLTSTQE---HILMLLAE----QISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRA  85
           +KL+S  E   ++L++LA     +  ++  +A +LK+SP+ + K +K L ++ L++S+
Sbjct  1   MKLSSGWEQSVYVLLILARLPENRTMSSIALANRLKVSPSYLKKIIKSLVDEGLLRSTTG  60

Query  86  TN  87
            N
Sbjct  61  KN  62
```

>**ref|YP_808573.1|** BadM/Rrf2 family transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
Length=156

GENE ID: 4433945 LACR_0579 | BadM/Rrf2 family transcriptional regulator
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 32.3 bits (72), Expect = 0.018, Method: Compositional matrix adjust.
Identities = 18/62 (29%), Positives = 38/62 (61%), Gaps = 7/62 (11%)

```
Query  33  VKLTSTQE---HILMLLAE----QISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRA  85
           +KL+S  E   ++L++LA     +  ++  +A +LK+SP+ + K +K L ++ L++S+
Sbjct  1   MKLSSGWEQSVYVLLILARLPENRTMSSIALANRLKVSPSYLKKIIKSLVDEGLLRSTTG  60

Query  86  TN  87
            N
Sbjct  61  KN  62
```

>**ref|NP_266714.1|** hypothetical protein L153086 [Lactococcus lactis subsp. lactis Il1403]
Length=156

GENE ID: 1114177 yffB | hypothetical protein
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 32.3 bits (72), Expect = 0.018, Method: Compositional matrix adjust.
Identities = 18/62 (29%), Positives = 38/62 (61%), Gaps = 7/62 (11%)

```
Query  33  VKLTSTQE---HILMLLAE----QISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRA  85
           +KL+S  E   ++L++LA     +  ++  +A +LK+SP+ + K +K L ++ L++S+
Sbjct  1   MKLSSGWEQSVYVLLILARLPENRTMSSIALANRLKVSPSYLKKIIKSLVDEGLLRSTPG  60

Query  86  TN  87
            N
Sbjct  61  KN  62
```

>**ref|YP_001033090.1|** MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]
Length=160

GENE ID: 4798315 rmaA | MarR family transcriptional regulator
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 31.6 bits (70), Expect = 0.031, Method: Compositional matrix adjust.
Identities = 29/107 (27%), Positives = 52/107 (48%), Gaps = 10/107 (9%)

```
Query  41   HILMLLAEQISTNA---KIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLT  97
            +L L++   I  N    +I + L I  ++V +A++ L E+E +   R  +D+R    SLT
Sbjct  42   QLLCLISLYIKDNQSQEQITDDLSIDKSSVHRAIRSLIEKEYVVRVRDEHDKRAYRVSLT  101

Query  98   EKAVPVAK--EHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTE  142
            +KA  +    E  T   + L     L      +E+E+  K L+ +T+
```

```
Sbjct  102  KKARAIQSQIEEMTKERENL-----LSEGIDPKEKEIAFKVLNQMTQ  143
```

>**ref|YP_808765.1|** MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
Length=155

GENE ID: 4432345 LACR_0786 | MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 31.6 bits (70), Expect = 0.034, Method: Compositional matrix adjust.
Identities = 20/65 (30%), Positives = 36/65 (55%), Gaps = 3/65 (4%)

```
Query  42   ILMLLAEQISTNA---KIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTE  98
            +L L++  I  N    +I + L I  ++V +A++ L E+E +   R  +D+R    SLT+
Sbjct  43   LLCLISLYIKDNQSQEQITDDLSIDKSSVHRAIRSLIEKEYVVRVRDEHDKRAYRVSLTK  102

Query  99   KAVPV  103
            KA  +
Sbjct  103  KARAI  107
```

>**ref|YP_808795.1|** MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
ref|YP_001033061.1| MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]
Length=146

GENE ID: 4433123 LACR_0820 | MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 31.2 bits (69), Expect = 0.044, Method: Compositional matrix adjust.
Identities = 19/57 (33%), Positives = 31/57 (54%), Gaps = 3/57 (5%)

```
Query  56   IAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHE  112
            IA+  K++ + +T  L +L+++  I+  R+T D RV    LT K   +    ATH E
Sbjct  57   IAKNQKLALSTITITLNRLEDKGYIERKRSTADRRVTHIILTSKGDELC---ATHRE  110
```

>**ref|NP_266926.1|** MarR family transcriptional regulator [Lactococcus lactis subsp. lactis Il1403]
Length=146

GENE ID: 1114397 rmaG | MarR family transcriptional regulator [Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 31.2 bits (69), Expect = 0.045, Method: Compositional matrix adjust.
Identities = 19/57 (33%), Positives = 31/57 (54%), Gaps = 3/57 (5%)

```
Query  56   IAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHE  112
            IA+  K++ + +T  L +L+++  I+  R+T D RV    LT K   +    ATH E
Sbjct  57   IAKNQKLALSTITITLNRLEDKGYIERKRSTADRRVTHIILTSKGDELC---ATHRE  110
```

>**ref|YP_001032909.1|** MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]
Length=154

GENE ID: 4797429 rmaH | MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 28.9 bits (63), Expect = 0.18, Method: Compositional matrix adjust.
Identities = 24/85 (28%), Positives = 41/85 (48%), Gaps = 1/85 (1%)

```
Query  54   AKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEK  113
            +KIA+    S A +   L  L+ + LI    +  D R +L ++T+K   VA+E
Sbjct  51   SKIAKFTHTSTARIATILNNLESKNLITREISRTDRRKILVAITDKGRRVAEEIRVEACS  110

Query  114  TLS-TYQELGNKFTDEEQEVISKFL  137
             L+  ++E+G + T+   E    FL
Sbjct  111  NLARVFKEMGEERTESFIENFKMFL  135
```

>**ref|YP_001032520.1|** MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]
Length=127

GENE ID: 4797914 rmaX | MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 28.1 bits (61), Expect = 0.31, Method: Compositional matrix adjust.
Identities = 24/86 (27%), Positives = 36/86 (41%), Gaps = 6/86 (6%)

```
Query  54   AKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEK  113
            + IA  +  S A V   L  L+E+ +I    +  D R +L  LT+K     KE  T
Sbjct  29   SDIARYIGASTARVANILNNLEEKGMISREISREDRRKILVFLTDKGRKETKERRTR---  85
```

```
Query  114  TLSTYQELGNKFTDEEQEVISKFLSA  139
            T   + N F    +E   +F+ A
Sbjct  86   ---TITRISNVFEAMGEERTQQFIEA  108
```

>ref|NP_267064.1| transcription regulator [Lactococcus lactis subsp. lactis Il1403]
Length=154

GENE ID: 1114538 rmaH | transcription regulator
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 28.1 bits (61), Expect = 0.35, Method: Compositional matrix adjust.
Identities = 23/85 (27%), Positives = 41/85 (48%), Gaps = 1/85 (1%)

```
Query  54   AKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEK  113
            +KIA+    S A +   L  L+ + L+    +  D R +L ++T+K   VA+E
Sbjct  51   SKIAKFTHTSTARIATILNNLESKNLVTREISRTDRRKILVAITDKGRHVAEEIRVEACS  110

Query  114  TLS-TYQELGNKFTDEEQEVISKFL  137
             L+  ++E+G + T+   E    FL
Sbjct  111  NLARVFEEMGEERTESFIENFKLFL  135
```

>ref|YP_001032533.1| transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]
Length=217

GENE ID: 4798916 llmg_1224 | transcriptional regulator
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 28.1 bits (61), Expect = 0.38, Method: Compositional matrix adjust.
Identities = 14/33 (42%), Positives = 24/33 (72%), Gaps = 1/33 (3%)

```
Query  48  EQISTNAKIAEKLKISPAAVTKALKKLQEQELI  80
           E +S NA IA+KL +S  + T+ +K+L ++EL+
Sbjct  23  ESVSINA-IAQKLSVSSPSATEMIKRLAKKELV  54
```

>ref|YP_809312.1| Mn-dependent transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
Length=217

GENE ID: 4432558 LACR_1369 | Mn-dependent transcriptional regulator
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 28.1 bits (61), Expect = 0.38, Method: Compositional matrix adjust.
Identities = 14/33 (42%), Positives = 24/33 (72%), Gaps = 1/33 (3%)

```
Query  48  EQISTNAKIAEKLKISPAAVTKALKKLQEQELI  80
           E +S NA IA+KL +S  + T+ +K+L ++EL+
Sbjct  23  ESVSINA-IAQKLSVSSPSATEMIKRLAKKELV  54
```

>ref|NP_267461.1| transcription regulator [Lactococcus lactis subsp. lactis Il1403]
Length=156

GENE ID: 1114954 rmaF | transcription regulator
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 27.7 bits (60), Expect = 0.42, Method: Compositional matrix adjust.
Identities = 15/45 (33%), Positives = 24/45 (53%), Gaps = 0/45 (0%)

```
Query  56   IAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKA  100
            + E L IS  A+   +  L+E+EL+      ND+R+    LTE+
Sbjct  63   LLEVLDISKQALNGPMNDLKEKELVHFKPNENDKRIKQLYLTEQG  107
```

>ref|NP_267696.1| transcription regulator [Lactococcus lactis subsp. lactis Il1403]
Length=148

GENE ID: 1115197 rmaI | transcription regulator
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 27.3 bits (59), Expect = 0.61, Method: Compositional matrix adjust.
Identities = 32/142 (22%), Positives = 60/142 (42%), Gaps = 18/142 (12%)

```
Query  11   LGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAK-------IAEKLKIS  63
            +G +++ A N+          + + LT  Q  IL  L  Q   ++        I  +  I
Sbjct  8    IGRLLKVASNQMSREFDNFAAQLDLTGQQMSILDFLGNQSEEDSGKEISQTMIELEFNIR  67

Query  64   PAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHAT----HHEKTLSTYQ  119
             +  T+ L+++++++LIK   +  D R     LTE+      E  T    H++K L+
Sbjct  68   RSTTTEILQRMEKRQLIKRKASPTDARQKSVELTEEGKQYLPEIRTYIQGHNQKALAG--  125

Query  120  ELGNKFTDEEQEVISKFLSALT  141
                + EE   + KFL+  +
Sbjct  126  -----LSAEEIAAVEKFLNNFS  142
```

Annex 2

>**ref|NP_266753.1|** NADPH-flavin oxidoreductase [Lactococcus lactis subsp. lactis Il1403]
Length=216

GENE ID: 1114217 yfiJ | NADPH-flavin oxidoreductase
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 27.3 bits (59), Expect = 0.67, Method: Compositional matrix adjust.
Identities = 11/29 (37%), Positives = 18/29 (62%), Gaps = 0/29 (0%)

```
Query  109  THHEKTLSTYQELGNKFTDEEQEVISKFL  137
            +HH+K+    QE+ N  T   +E ++KFL
Sbjct  180  SHHQKSTDWTQEMSNFLTKPRREDVAKFL  208
```

>**ref|NP_267412.1|** metalloregulator [Lactococcus lactis subsp. lactis Il1403]
Length=217

GENE ID: 1114905 ymiA | metalloregulator
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 26.6 bits (57), Expect = 1.1, Method: Compositional matrix adjust.
Identities = 13/31 (41%), Positives = 23/31 (74%), Gaps = 1/31 (3%)

```
Query  50  ISTNAKIAEKLKISPAAVTKALKKLQEQELI  80
           +S NA IA+KL +S  + T+ +K+L ++EL+
Sbjct  25  VSINA-IAQKLSVSSPSATEMIKRLAKKELV  54
```

>**ref|YP_001031697.1|** putative cobalt ABC transporter ATP-binding protein [Lactococcus lactis subsp. cremoris MG1363]
Length=565

GENE ID: 4798558 cbiO | putative cobalt ABC transporter ATP-binding protein
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 26.2 bits (56), Expect = 1.2, Method: Compositional matrix adjust.
Identities = 12/27 (44%), Positives = 17/27 (62%), Gaps = 0/27 (0%)

```
Query  55   KIAEKLKISPAAVTKALKKLQEQELIK  81
            ++A K  ISP ++TKA    Q QE +K
Sbjct  537  QLARKADISPISLTKAFINFQNQERLK  563
```

>**ref|NP_266873.1|** quinone oxidoreductase [Lactococcus lactis subsp. lactis Il1403]
Length=328

GENE ID: 1114342 qor | quinone oxidoreductase
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 25.4 bits (54), Expect = 2.4, Method: Compositional matrix adjust.
Identities = 10/19 (52%), Positives = 11/19 (57%), Gaps = 0/19 (0%)

```
Query  109  THHEKTLSTYQELGNKFTD  127
             HHEK +    ELG KF D
Sbjct  193  NHHEKLVPQVHELGFKFVD  211
```

>**ref|NP_268402.1|** alkylphosphonate uptake protein [Lactococcus lactis subsp. lactis Il1403]
Length=114

GENE ID: 1115923 phnA | alkylphosphonate uptake protein
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 25.4 bits (54), Expect = 2.4, Method: Compositional matrix adjust.
Identities = 14/41 (34%), Positives = 19/41 (46%), Gaps = 0/41 (0%)

```
Query  97   TEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFL  137
            T K +  + E+      T     E GN+FT EE E   KF+
Sbjct  3    TPKCIHCSSEYTYELSDTSFGCSECGNEFTLEEIEAAGKFI  43
```

>**ref|YP_808209.1|** transcriptional repressor CodY [Lactococcus lactis subsp. cremoris SK11]
Length=262

GENE ID: 4434653 LACR_0168 | transcriptional repressor CodY
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 24.6 bits (52), Expect = 3.4, Method: Compositional matrix adjust.
Identities = 10/27 (37%), Positives = 19/27 (70%), Gaps = 0/27 (0%)

```
Query  56   IAEKLKISPAAVTKALKKLQEQELIKS  82
            IA+K+ I+ + +  AL+KL+   +I+S
```

```
Sbjct  210  IADKIGITRSVIVNALRKLESAGVIES  236
```

>ref|YP_001031533.1| transcriptional repressor CodY [Lactococcus lactis subsp. cremori MG1363]
Length=262

GENE ID: 4797198 codY | transcriptional repressor CodY
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 24.6 bits (52), Expect = 3.4, Method: Compositional matrix adjust.
Identities = 10/27 (37%), Positives = 19/27 (70%), Gaps = 0/27 (0%)

```
Query  56   IAEKLKISPAAVTKALKKLQEQELIKS  82
            IA+K+ I+ + +  AL+KL+   +I+S
Sbjct  210  IADKIGITRSVIVNALRKLESAGVIES  236
```

>ref|NP_266317.1| transcriptional repressor CodY [Lactococcus lactis subsp. lactis Il1403]
Length=262

GENE ID: 1113769 codY | transcriptional repressor CodY
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 24.6 bits (52), Expect = 3.5, Method: Compositional matrix adjust.
Identities = 10/27 (37%), Positives = 19/27 (70%), Gaps = 0/27 (0%)

```
Query  56   IAEKLKISPAAVTKALKKLQEQELIKS  82
            IA+K+ I+ + +  AL+KL+   +I+S
Sbjct  210  IADKIGITRSVIVNALRKLESAGVIES  236
```

>ref|NP_266838.1| intercellular adhesion protein [Lactococcus lactis subsp. lactis Il1403]
Length=276

GENE ID: 1114306 icaB | intercellular adhesion protein
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 24.6 bits (52), Expect = 3.6, Method: Compositional matrix adjust.
Identities = 14/46 (30%), Positives = 21/46 (45%), Gaps = 0/46 (0%)

```
Query  43   LMLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATND  88
            L L   Q     K+ + +  S  +  K +KK+ E  L+ S   TND
Sbjct  126  LDLPFTQFIITGKVGQTIDGSQMSTWKEIKKMNENPLVTSGLHTND  171
```

>ref|NP_266710.1| transcription regulator [Lactococcus lactis subsp. lactis Il1403]
Length=247

GENE ID: 1114173 yfeA | transcription regulator
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 24.6 bits (52), Expect = 3.6, Method: Compositional matrix adjust.
Identities = 16/44 (36%), Positives = 25/44 (56%), Gaps = 5/44 (11%)

```
Query  35  LTSTQEHILMLLAEQIS-----TNAKIAEKLKISPAAVTKALKK  73
           LTS + +I   L E  +     T A+IAE   +SP+++ + LKK
Sbjct  4   LTSVEIYIWNYLEENKAKIIQMTVAQIAESAHVSPSSIIRTLKK  47
```

>ref|NP_266438.1| amino acid amidohydrolase [Lactococcus lactis subsp. lactis Il1403]
Length=384

GENE ID: 1113892 yciA | amino acid amidohydrolase
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 24.6 bits (52), Expect = 4.1, Method: Compositional matrix adjust.
Identities = 11/41 (26%), Positives = 17/41 (41%), Gaps = 7/41 (17%)

```
Query  8    DQFLGT-------IMQFAENKHEILLGKCESDVKLTSTQEH  41
            D+F G         +   A N+H +  G CE ++    T  H
Sbjct  147  DEFYGLHVRPDLKVGDIATNQHTLFAGTCEVELSFIGTGGH  187
```

>ref|YP_808446.1| lysyl-tRNA synthetase [Lactococcus lactis subsp. cremoris SK11]
Length=494

GENE ID: 4433352 lysS | lysyl-tRNA synthetase
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 24.6 bits (52), Expect = 4.3, Method: Composition-based stats.
Identities = 12/34 (35%), Positives = 20/34 (58%), Gaps = 0/34 (0%)

```
Query  98   EKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQE  131
            E+A  +AKEH  H EK  ++   + N+F ++  E
```

```
Sbjct  340  EEATALAKEHDIHVEKHFTSVGHIINEFFEKYVE  373
```

>ref|YP_001031741.1| lysyl-tRNA synthetase [Lactococcus lactis subsp. cremoris MG1363]
Length=494

GENE ID: 4799123 lysS | lysyl-tRNA synthetase
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 24.3 bits (51), Expect = 4.7, Method: Composition-based stats.
Identities = 12/34 (35%), Positives = 20/34 (58%), Gaps = 0/34 (0%)

```
Query  98   EKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQE  131
            E+A  +AKEH  H EK  ++   + N+F ++  E
Sbjct  340  EEATALAKEHDIHVEKHFTSVGHIINEFFEKYVE  373
```

>ref|NP_266529.1| lysyl-tRNA synthetase [Lactococcus lactis subsp. lactis Il1403]
Length=494

GENE ID: 1113984 lysS | lysyl-tRNA synthetase
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 24.3 bits (51), Expect = 4.7, Method: Composition-based stats.
Identities = 12/34 (35%), Positives = 20/34 (58%), Gaps = 0/34 (0%)

```
Query  98   EKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQE  131
            E+A  +AKEH  H EK  ++   + N+F ++  E
Sbjct  340  EEATALAKEHDIHVEKHFTSVGHIINEFFEKYVE  373
```

>ref|YP_001031907.1| NADPH-flavin oxidoreductase [Lactococcus lactis subsp. cremoris MG1363]
Length=251

GENE ID: 4798593 llmg_0559 | NADPH-flavin oxidoreductase
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 24.3 bits (51), Expect = 5.2, Method: Compositional matrix adjust.
Identities = 9/29 (31%), Positives = 19/29 (65%), Gaps = 0/29 (0%)

```
Query  109  THHEKTLSTYQELGNKFTDEEQEVISKFL  137
            +HH+K+ +  QE+ +  T+  +E ++ FL
Sbjct  215  SHHQKSTNWSQEMSDFLTNPRREDLTDFL  243
```

>ref|YP_808603.1| NADPH-flavin oxidoreductase [Lactococcus lactis subsp. cremoris SK11]
Length=251

GENE ID: 4433732 LACR_0613 | NADPH-flavin oxidoreductase
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 24.3 bits (51), Expect = 5.5, Method: Compositional matrix adjust.
Identities = 9/29 (31%), Positives = 19/29 (65%), Gaps = 0/29 (0%)

```
Query  109  THHEKTLSTYQELGNKFTDEEQEVISKFL  137
            +HH+K+ +  QE+ +  T+  +E ++ FL
Sbjct  215  SHHQKSTNWSQEMSDFLTNPRREDLADFL  243
```

>ref|NP_268293.1| exported serine protease [Lactococcus lactis subsp. lactis Il1403]
Length=408

GENE ID: 1115813 htrA | exported serine protease
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 23.9 bits (50), Expect = 6.1, Method: Compositional matrix adjust.
Identities = 17/59 (28%), Positives = 34/59 (57%), Gaps = 5/59 (8%)

```
Query  15   MQFAENKHEI--LLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKISPAAVTKAL  71
            + FA   +++  ++ K E+D K++      I M+   Q+STN   + +LK+ P++VT  +
Sbjct  271  LGFAIPSNDVVNIINKLEADGKISRPALGIRMVDLSQLSTND--SSQLKL-PSSVTGGV  326
```

>ref|YP_001033660.1| housekeeping protease [Lactococcus lactis subsp. cremoris MG1363]
Length=407

GENE ID: 4797497 htrA | housekeeping protease
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 23.9 bits (50), Expect = 6.5, Method: Compositional matrix adjust.
Identities = 17/59 (28%), Positives = 34/59 (57%), Gaps = 5/59 (8%)

```
Query  15   MQFAENKHEI--LLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKISPAAVTKAL  71
            + FA   +++  ++ K E+D K++      I M+   Q+STN   + +LK+ P++VT  +
Sbjct  270  LGFAIPSNDVVNIINKLETDGKISRPALGIRMVDLSQLSTND--SSQLKL-PSSVTGGV  325
```

Annex 2

>**ref|YP_811995.1|** trypsin-like serine protease [Lactococcus lactis subsp. cremoris SK11]
Length=407

GENE ID: 4432303 LACR_2439 | trypsin-like serine protease
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 23.9 bits (50), Expect = 6.6, Method: Compositional matrix adjust.
Identities = 17/59 (28%), Positives = 34/59 (57%), Gaps = 5/59 (8%)

```
Query  15   MQFAENKHEI--LLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKISPAAVTKAL  71
            + FA   +++  ++ K E+D K++     I M+   Q+STN   + +LK+ P++VT  +
Sbjct  270  LGFAIPSNDVVNIINKLETDGKISRPALGIRMVDLSQLSTND--SSQLKL-PSSVTGGV  325
```

>**ref|NP_268332.1|** hypothetical protein L35545 [Lactococcus lactis subsp. lactis Il1403]
ref|YP_812032.1| hypothetical protein LACR_2483 [Lactococcus lactis subsp. cremoris SK11]
ref|YP_001033699.1| hypothetical protein llmg_2459 [Lactococcus lactis subsp. cremori MG1363]
Length=82

GENE ID: 1115852 ywfB | hypothetical protein
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 23.5 bits (49), Expect = 7.5, Method: Compositional matrix adjust.
Identities = 13/29 (44%), Positives = 14/29 (48%), Gaps = 0/29 (0%)

```
Query  97   TEKAVPVAKEHATHHEKTLSTYQELGNKF  125
            TE     AKE A  +E  L  YQ L  KF
Sbjct  34   TEDGKKEAKEAAIRYESRLDAYQFLQGKF  62
```

>**ref|NP_268337.1|** hypothetical protein L39650 [Lactococcus lactis subsp. lactis Il1403]
Length=926

GENE ID: 1115857 ywfG | hypothetical protein
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 23.5 bits (49), Expect = 7.7, Method: Composition-based stats.
Identities = 11/25 (44%), Positives = 13/25 (52%), Gaps = 0/25 (0%)

```
Query  118  YQELGNKFTDEEQEVISKFLSALTE  142
            Y E G KF D+ Q  I +    LTE
Sbjct  557  YPEDGTKFADDPQHYIVRLKHGLTE  581
```

>**ref|YP_001032772.1|** superfamily II DNA/RNA helicase [Lactococcus lactis subsp. cremoi MG1363]
Length=430

GENE ID: 4797767 comFA | superfamily II DNA/RNA helicase
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 23.5 bits (49), Expect = 7.8, Method: Compositional matrix adjust.
Identities = 17/46 (36%), Positives = 26/46 (56%), Gaps = 1/46 (2%)

```
Query  34   KLTSTQEHILMLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQEL  79
            KLT  QE I   L +QI+ N K+  +  ++ A  T+ + +L EQ L
Sbjct  105  KLTENQEKISNALCQQITNNQKLLVQ-AVTGAGKTEMIYQLIEQIL  149
```

>**ref|YP_001033122.1|** quinone oxidoreductase [Lactococcus lactis subsp. cremoris MG1363
Length=328

GENE ID: 4798878 qor | quinone oxidoreductase
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 23.5 bits (49), Expect = 9.3, Method: Compositional matrix adjust.
Identities = 9/18 (50%), Positives = 10/18 (55%), Gaps = 0/18 (0%)

```
Query  110  HHEKTLSTYQELGNKFTD  127
            HHE  +    ELG KF D
Sbjct  194  HHENLVPQVHELGFKFVD  211
```

>**ref|YP_808733.1|** quinone oxidoreductase [Lactococcus lactis subsp. cremoris SK11]
Length=328

GENE ID: 4432226 LACR_0751 | quinone oxidoreductase
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 23.5 bits (49), Expect = 9.3, Method: Compositional matrix adjust.
Identities = 9/18 (50%), Positives = 10/18 (55%), Gaps = 0/18 (0%)

```
Query  110  HHEKTLSTYQELGNKFTD  127
            HHE  +    ELG KF D
Sbjct  194  HHENLVPQVHELGFKFVD  211
```

>ref|YP_796521.1| hypothetical protein LACR_C57 [Lactococcus lactis subsp. cremoris SK11]
Length=330

GENE ID: 4405852 LACR_C57 | hypothetical protein
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 23.5 bits (49), Expect = 9.5, Method: Compositional matrix adjust.
Identities = 11/33 (33%), Positives = 22/33 (66%), Gaps = 0/33 (0%)

```
Query  53   NAKIAEKLKISPAAVTKALKKLQEQELIKSSRA  85
            N K  ++L  S +  ++A  K+Q Q+L+K+S++
Sbjct  189  NIKDTQELDFSSSNFSEAQLKVQNQDLVKNSKS  221
```

>ref|YP_812095.1| hypothetical protein LACR_2554 [Lactococcus lactis subsp. cremoris SK11]
Length=114

GENE ID: 4432134 LACR_2554 | hypothetical protein
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 23.1 bits (48), Expect = 10.0, Method: Compositional matrix adjust.
Identities = 13/41 (31%), Positives = 18/41 (43%), Gaps = 0/41 (0%)

```
Query  97   TEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFL  137
            T K +  + E+            E GN+FT EE E   KF+
Sbjct  3    TPKCIHCSSEYTYELSDMSFGCSECGNEFTLEEIEAAGKFI  43
```

Select All Get selected sequences Distance tree of results

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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/525,449	11/09/2005	Isabelle Poquet	1169-034	3827

20529 7590 07/07/2009

THE NATH LAW GROUP
112 South West Street
Alexandria, VA 22314

EXAMINER	
MARVICH, MARIA	
ART UNIT	**PAPER NUMBER**
1633	

MAIL DATE	DELIVERY MODE
07/07/2009	PAPER

Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Notice of Non-Compliant Amendment (37 CFR 1.121)	Application No.	Applicant(s)	
	10/525,449	POQUET ET AL.	
	Examiner	Art Unit	
	MARIA B. MARVICH	1633	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

The amendment document filed on _____ is considered non-compliant because it has failed to meet the requirements of 37 CFR 1.121 or 1.4. In order for the amendment document to be compliant, correction of the following item(s) is required.

THE FOLLOWING MARKED (X) ITEM(S) CAUSE THE AMENDMENT DOCUMENT TO BE NON-COMPLIANT:

- ☐ 1. Amendments to the specification:
  - ☐ A. Amended paragraph(s) do not include markings.
  - ☐ B. New paragraph(s) should not be underlined.
  - ☐ C. Other _____.
- ☐ 2. Abstract:
  - ☐ A. Not presented on a separate sheet. 37 CFR 1.72.
  - ☐ B. Other _____.
- ☐ 3. Amendments to the drawings:
  - ☐ A. The drawings are not properly identified in the top margin as "Replacement Sheet," "New Sheet," or "Annotated Sheet" as required by 37 CFR 1.121(d).
  - ☐ B. The practice of submitting proposed drawing correction has been eliminated. Replacement drawings showing amended figures, without markings, in compliance with 37 CFR 1.84 are required.
  - ☐ C. Other _____.
- ☒ 4. Amendments to the claims:
  - ☐ A. A complete listing of all of the claims is not present.
  - ☐ B. The listing of claims does not include the text of all pending claims (including withdrawn claims)
  - ☒ C. Each claim has not been provided with the proper status identifier, and as such, the individual status of each claim cannot be identified. Note: the status of every claim must be indicated after its claim number by using one of the following status identifiers: (Original), (Currently amended), (Canceled), (Previously presented), (New), (Not entered), (Withdrawn) and (Withdrawn-currently amended).
  - ☐ D. The claims of this amendment paper have not been presented in ascending numerical order.
  - ☒ E. Other: *See Continuation Sheet*.
- ☐ 5. Other (e.g., the amendment is unsigned or not signed in accordance with 37 CFR 1.4):

_____

For further explanation of the amendment format required by 37 CFR 1.121, see MPEP § 714.

TIME PERIODS FOR FILING A REPLY TO THIS NOTICE:

1. Applicant is given **no new time period** if the non-compliant amendment is an after-final amendment or an amendment filed after allowance. If applicant wishes to resubmit the non-compliant after-final amendment with corrections, the **entire corrected amendment** must be resubmitted.
2. Applicant is given **one month**, or thirty (30) days, whichever is longer, from the mail date of this notice to supply the correction, if the non-compliant amendment is one of the following: a preliminary amendment, a non-final amendment (including a submission for a request for continued examination (RCE) under 37 CFR 1.114), a supplemental amendment filed within a suspension period under 37 CFR 1.103(a) or (c), and an amendment filed in response to a *Quayle* action. If any of above boxes 1. to 4. are checked, the correction required is only the **corrected section** of the non-compliant amendment in compliance with 37 CFR 1.121.

   Extensions of time are available under 37 CFR 1.136(a) only if the non-compliant amendment is a non-final amendment or an amendment filed in response to a *Quayle* action.

   Failure to timely respond to this notice will result in:
   Abandonment of the application if the non-compliant amendment is a non-final amendment or an amendment filed in response to a *Quayle* action; or
   Non-entry of the amendment if the non-compliant amendment is a preliminary amendment or supplemental amendment.

/Maria B Marvich/ Primary Examiner, Art Unit 1633	

Continuation of 4(e) Other: Clam 13 indicates that it is previously presented, however, amendment has been made to delete the phrase "in which TATAAT represents the -10 box of said promoter" without markings.

As well, the objections to the claims and rejections under 35 USC 112, first paragraph made in the office action mailed 10/7/08 have not been addressed in the repsonse mailed 4/7/09. For example, the objection to claim 16 and 18 for reference to a previous claim using the artilce "an" as opposed to "the" has not been addressed. by amendment or argument. Similarly, the objection to claims i.e. 20 for recitation of at least one has not been addressed. Recommendation has been made to use the artilce "the" as opposed to "at least one". Claim 15 has been objected to as being a duplicate of claim 12, however, applicants have not addressed this objection. Finally, the rejection under 35 USC 112, first paragraph has not been addressed.

NATH & ASSOCIATES, PLLC
DBA: THE NATH LAW GROUP

8108

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Patent Office Fee Serial No. 10/525,449

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